

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 24, 2004, 12:46:54 ; Search time 3 Seconds
(without alignments)
4.063 Million cell updates/sec

Title: frags1-16

Perfect score: 1122

Sequence: 1 cgtctcttcttcggtcct.....aggccgcaggaggaagc 1122

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 329 seqs, 5432 residues

Total number of hits satisfying chosen parameters: 658

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 637 summaries

Database : rng1-16.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	30	2.7	30	1 AAV63648	Antisense oligonuc
C 2	30	2.7	30	1 AAV63649	Antisense oligonuc
C 3	30	2.7	30	1 AAV63649	Antisense oligonuc
C 4	30	2.7	30	1 AAV41175	RNA component of h
C 5	30	2.7	30	1 AAV41175	RNA component of h
C 6	30	2.7	30	1 AAV41169	RNA component of h
C 7	30	2.7	30	1 AAV41172	RNA component of h
C 8	30	2.7	30	1 AAV41172	RNA component of h
C 9	30	2.7	30	1 AAZ23630	Human clone 28-1 t
C 10	30	2.7	30	1 AAZ23631	Human clone 28-1 t
C 11	30	2.7	30	1 AAZ23631	Human clone 28-1 t
C 12	30	2.7	30	1 AAS15928	Human telomerase p
C 13	30	2.7	30	1 AAS15928	Human telomerase p
C 14	30	2.7	30	1 AAS09476	Antisense oligonuc
C 15	30	2.7	30	1 AAS09476	Antisense oligonuc
C 16	30	2.7	30	1 AAS09475	Antisense oligonuc
C 17	30	2.7	30	1 ABA91517	Oligonucleotide us
C 18	30	2.7	30	1 ABA91517	Oligonucleotide us
C 19	30	2.7	30	1 ABX10985	Human telomerase a
C 20	30	2.7	30	1 ABX10986	Human telomerase a
C 21	30	2.7	30	1 ABX10986	Human telomerase a
C 22	30	2.7	30	1 ABC35652	Human telomerase R
C 23	30	2.7	30	1 ABC35652	Human telomerase R
C 24	30	2.7	30	1 ABC35651	Human telomerase R
C 25	30	2.7	30	1 ABC35651	Human telomerase R
C 26	30	2.7	30	1 ADG62873	Human telomerase R
C 27	30	2.7	30	1 ADG62874	Human telomerase R
C 28	27	2.4	27	1 AAV41193	RNA component of h
C 29	27	2.4	27	1 ABA93497	Primer for product
C 30	26	2.3	26	1 AAT10304	RNA component of h
C 31	26	2.3	26	1 AAT10304	RNA component of h
C 32	26	2.3	26	1 AAT10299	RNA component of h
C 33	26	2.3	26	1 AAT58811	Human telomerase p

C 34	26	2.3	26	1 AAV17033	Telomerase PCR pri
C 35	26	2.3	26	1 AAV19489	Human htr gene R
C 36	26	2.3	26	1 AAX30788	Human telomerase R
C 37	26	2.3	26	1 AAX77402	PCR primer for Hum
C 38	26	2.3	26	1 AAX01542	Human telomerase R
C 39	26	2.3	26	1 AAX88250	Human telomerase R
C 40	26	2.3	26	1 ABK48024	Human telomerase (
C 41	26	2.3	26	1 AAD24246	Human telomerase (
C 42	26	2.3	26	1 ADG82593	Human telomerase p
C 43	25	2.2	25	1 AAC93100	RNA component of h
C 44	24	2.2	24	1 AAV41169	Human telomerase R
C 45	24	2.1	25	1 AAZ08704	Human telomerase R
C 46	23	2.0	23	1 ADF93794	Human TERC mRNA tr
C 47	23	2.0	23	1 ADF93793	Human TERC mRNA tr
C 48	23	2.0	23	1 ADF93793	Human TERC mRNA tr
C 49	23	2.0	23	1 ADG29525	htr siNA-target RN
C 50	23	2.0	23	1 ADG29524	htr siNA-target RN
C 51	23	2.0	23	1 ADG29524	htr siNA-target RN
C 52	23	2.0	27	1 AAV41193	RNA component of h
C 53	23	2.0	27	1 ABA95497	Human telomerase R
C 54	22	2.0	22	1 AAT58812	Human telomerase p
C 55	22	2.0	23	1 ADF93795	Human TERC mRNA tr
C 56	22	2.0	23	1 ADF93795	Human TERC mRNA tr
C 57	22	2.0	23	1 ADF93802	Human TERC mRNA tr
C 58	22	2.0	23	1 ADF93802	Human TERC mRNA tr
C 59	22	2.0	23	1 ADG29526	htr siNA-target RN
C 60	22	2.0	23	1 ADG29526	htr siNA-target RN
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C 62	22	2.0	23	1 ADG29520	htr siNA-target RN
C 63	22	2.0	25	1 AAZ08704	Human telomerase R
C 64	22	2.0	25	1 AAZ07280	Human telomerase R
C 65	22	2.0	26	1 AAT11044	Primer for product
C 66	22	2.0	26	1 AAT10304	RNA component of h
C 67	22	2.0	26	1 AAT10299	RNA component of h
C 68	22	2.0	26	1 AAT58811	Human telomerase p
C 69	22	2.0	26	1 AAV17033	Telomerase PCR pri
C 70	22	2.0	26	1 AAV19489	Human htr gene R
C 71	22	2.0	26	1 AAX90788	Human telomerase R
C 72	22	2.0	26	1 AAX77402	PCR primer for Hum
C 73	22	2.0	26	1 AAX01542	Human telomerase R
C 74	22	2.0	26	1 AAX88250	Human telomerase R
C 75	22	2.0	26	1 ABK48024	Human telomerase (
C 76	22	2.0	26	1 AAD24246	Human telomerase (
C 77	22	2.0	26	1 ADG82593	Human telomerase p
C 78	21	1.9	21	1 ADF93860	Human TERC siRNA,
C 79	21	1.9	21	1 ADF93860	Human TERC siRNA,
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C 81	21	1.9	21	1 ADG30029	htr-targeted siNA,
C 82	21	1.9	22	1 ACC57544	Telomerase PCR pri
C 83	21	1.9	22	1 ACC57544	Telomerase PCR pri
C 84	21	1.9	23	1 ADF93794	Human TERC mRNA tr
C 85	21	1.9	23	1 ADG29525	htr siNA-target RN
C 86	20	1.8	20	1 AAV71226	Antisense oligonuc
C 87	20	1.8	20	1 AAV71226	Antisense oligonuc
C 88	20	1.8	20	1 AAV41173	RNA component of h
C 89	20	1.8	20	1 AAV41173	RNA component of h
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C 91	20	1.8	20	1 AAV41170	RNA component of h
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C 94	20	1.8	20	1 AAV41180	RNA component of h
C 95	20	1.8	20	1 AAV41180	RNA component of h
C 96	20	1.8	20	1 AAZ23632	Human clone 28-1 t
C 97	20	1.8	20	1 AAZ23632	Human clone 28-1 t
C 98	20	1.8	20	1 AAZ23632	Human clone 28-1 t
C 99	20	1.8	20	1 AAZ23636	Human clone 28-1 t
C 100	20	1.8	20	1 AAZ23636	Human clone 28-1 t
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C 102	20	1.8	20	1 AAS09477	Antisense oligonuc
C 103	20	1.8	20	1 AAS09477	Antisense oligonuc
C 104	20	1.8	20	1 AAS09480	Antisense oligonuc
C 105	20	1.8	20	1 ADF93865	Human TERC siRNA,
C 106	20	1.8	21	1 ADF93865	Human TERC siRNA,

C 399	11	1.0	12	1	ABH79336	Oligonucleotide pr
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C 402	11	1.0	12	1	ABH86639	Oligonucleotide pr
C 403	11	1.0	12	1	ABH86639	Oligonucleotide pr
C 404	11	1.0	12	1	ABH933281	Oligonucleotide pr
C 405	11	1.0	12	1	ABH933281	Oligonucleotide pr
C 406	11	1.0	12	1	ACA62980	Tandem N-box probe
C 407	11	1.0	12	1	ACA62980	Tandem N-box probe
C 408	11	1.0	12	1	ACA00988	Mouse DNA containi
C 409	11	1.0	12	1	ADA00988	Mouse DNA containi
C 410	11	1.0	12	1	ADD10236	GA binding protein
C 411	11	1.0	12	1	ADD10236	GA binding protein
C 412	11	1.0	12	1	ABF44983	Oligonucleotide SE
C 413	11	1.0	12	1	ABF44983	Oligonucleotide SE
C 414	11	1.0	12	1	ABF44982	Oligonucleotide SE
C 415	11	1.0	12	1	AXA00290	Target DNA sequenc
C 416	11	1.0	12	1	ABC68546	Oligonucleotide SE
C 417	11	1.0	12	1	ABC68546	Oligonucleotide SE
C 418	11	1.0	12	1	ABC68546	Oligonucleotide SE
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C 429	11	1.0	12	1	ABH49432	Oligonucleotide SE
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C 431	11	1.0	12	1	ABH49433	Oligonucleotide SE
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C 451	11	1.0	12	1	ABC79044	Oligonucleotide SE
C 452	11	1.0	12	1	ABC79044	Oligonucleotide SE
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C 463	11	1.0	12	1	ABC49396	Oligonucleotide SE
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C 470	11	1.0	12	1	ASC10396	Oligonucleotide SE
C 471	11	1.0	12	1	ABF11407	Oligonucleotide SE

[illegible]

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 07:29:59 ; Search time 0.001 Seconds
(without alignments)
1.596 Million cell updates/sec

Title: US-09-436-060A-12

Perfect score: 7
Sequence: 1 gctctag 7

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 14 seqs, 114 residues

Total number of hits satisfying chosen parameters: 28

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 19 summaries

Database : rge12.seq*

Pred. No. is the number of results predicted by chance, to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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7	6	85.7	8	1	ACCSSION:BD023708
8	6	85.7	8	1	ACCSSION:BD023708
9	6	85.7	8	1	ACCSSION:BD023708
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18	6	85.7	8	1	ACCSSION:BD023708
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ALIGNMENTS

RESULT 1
BD023708
LOCUS BD023708 7 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for detecting and inhibiting RNA component of telomerase.
ACCESSION BD023708
VERSION BD023708.1 GI:22564931
KEYWORDS JP 2001507229-A/12.
SOURCE unidentified
ORGANISM unidentified

unclassified.

1 (bases 1 to 7)

AUTHORS Kim N.W., Wu F., Kealey, J.T., Pruzan, R. and Weinrich, S.L.
TITLE Method for detecting and inhibiting RNA component of telomerase
JOURNAL Patent JP 2001507229-A 12 05-JUN-2001;
COMMENT GERON CORP

PN JP 2001507229-A/12

PD 05-JUN-2001

PF 19-DEC-1997 JP 1998529003

PR 20-DEC-1996 US 08/770564, 20-DEC-1996 US 08/770565 PI

NAM WOO KIM, FRED WU, JAMES T KEALEY, RONALD PRUZAN, SCOTT L PI

WEINRICH

PC C12N15/09, A61K9/08, A61K31/7105, A61K45/00, A61K48/00, A61P35/00,

PC C12N5/10,

PC C12N9/12, C12Q1/68, C12Q1/68, C12N15/00, C12N5/00 CC

Strandedness: Single;

CC Topology: Linear;

CC /note= 'oligo 21ab1'

PH Key Location/Qualifiers.

source 1..7 Location/Qualifiers

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

Query Match 100.0%; Score 7; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAG 7

Db 1 GCTCTAG 7

RESULT 2

A83648

LOCUS A83648 9 bp DNA linear PAT 21-JAN-2000

DEFINITION Sequence 4 from Patent WO9849309.

ACCESSION A83648

VERSION A83648.1 GI:6732898

KEYWORDS

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 9)

Utans-Schneitz, U. and Lesslauer, W.

RAT ST38.2 CHEMOKINE

Patent: WO 9849309-A 4 05-NOV-1998;

HOFFMANN LA ROCHE (CH)

Location/Qualifiers

source 1..9

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

Query Match 100.0%; Score 7; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAG 7

Db 1 GCTCTAG 7

RESULT 3

BD106461

LOCUS BD106461 9 bp DNA linear PAT 18-SEP-2002

DEFINITION Rat ST38.2 chemokine.

ACCESSION BD106461

VERSION BD106461.1 GI:23201279

KEYWORDS JP 2002500509-A/2.

SOURCE Chlamydia sp.

ORGANISM Chlamydia sp.

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OM nucleic - nucleic search, using sw model

Run on: November 24, 2004, 12:41:14 ; Search time 1 Seconds
(without alignments)
6.384 Million cell updates/sec

Title: frags1-16
Perfect score: 1122
Sequence: 1 cgtctctctctctgagcct.....aggccgcaggaggaagc 1122

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 153 seqs, 2845 residues

Total number of hits satisfying chosen parameters: 306

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 306 summaries

Database : rge1-16.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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30	29	2.6	30	1	AR063832
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32	27	2.4	27	1	AR063832
33	26	2.3	26	1	AR063832

C 34	26	2.3	26	1	AR016055
C 35	26	2.3	26	1	AR028786
C 36	26	2.3	26	1	AR059216
C 37	26	2.3	26	1	AR075527
C 38	26	2.3	26	1	AR161925
C 39	26	2.3	26	1	BD176166
C 40	26	2.3	26	1	E36508
C 41	26	2.3	26	1	E37046
C 42	26	2.3	26	1	E37046
C 43	26	2.3	26	1	E37046
C 44	26	2.3	26	1	AR243519
C 45	26	2.3	26	1	AR306473
C 46	26	2.3	26	1	AR369723
C 47	26	2.3	26	1	AR370169
C 48	26	2.3	26	1	AR381130
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C 93	26	2.3	26	1	AR393335
C 94	26	2.3	26	1	AR393335
C 95	26	2.3	26	1	AR393335
C 96	26	2.3	26	1	AR393335
C 97	26	2.3	26	1	AR393335
C 98	26	2.3	26	1	AR393335
C 99	26	2.3	26	1	AR393335
C 100	26	2.3	26	1	AR393335
C 101	26	2.3	26	1	AR393335
C 102	26	2.3	26	1	AR393335
C 103	26	2.3	26	1	AR393335
C 104	26	2.3	26	1	AR393335
C 105	26	2.3	26	1	AR393335
C 106	26	2.3	26	1	AR393335

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OM.nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:41:42 ; Search time 0.001 Seconds
(without alignments)
37.880 Million cell updates/

Title: US-09-436-060A-3
Perfect score: 20
Sequence: 1 cgttcctcttctctgagcct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 89 seqs, 947 residues

Total number of hits satisfying chosen parameters: 178

Minimum DB seq	length: 7
Maximum DB seq	length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : rnpb3.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	15.8	79.0	20	1	US-10-174-020-71	Sequence 71, Appl
2	15.8	79.0	20	1	US-10-174-020-138	Sequence 138, Appl
C 3	12.8	64.0	17	1	US-09-780-533A-58	Sequence 58, Appl
4	12.8	64.0	17	1	US-09-780-533A-59	Sequence 59, Appl
5	12.8	64.0	17	1	US-10-138-674-8374	Sequence 8374, Ap
6	12.8	64.0	17	1	US-10-287-949A-8374	Sequence 8374, Ap
7	12.8	64.0	17	1	US-10-287-949A-8374	Sequence 8374, Ap
C 8	11.8	59.0	15	1	US-10-712-633-3415	Sequence 3415, Ap
C 9	11	55.0	12	1	US-10-182-233-68	Sequence 68, Appl
C 10	10	50.0	11	1	US-09-338-744-2	Sequence 2, Appl
11	9.4	47.0	11	1	US-10-670-011-393	Sequence 393, App
12	9.4	47.0	11	1	US-09-888-164-33	Sequence 33, Appl
13	9.4	47.0	11	1	US-09-793-146-41	Sequence 41, Appl
14	9.4	47.0	11	1	US-09-793-146-59	Sequence 59, Appl
15	9.4	47.0	11	1	US-09-793-146-60	Sequence 60, Appl
C 16	9.4	47.0	12	1	US-10-450-797-1093	Sequence 1093, Ap
C 17	9.4	47.0	12	1	US-09-835-370-62	Sequence 62, Appl
C 18	9	45.0	10	1	US-10-091-281-383	Sequence 383, App
C 19	9	45.0	10	1	US-09-884-363-10	Sequence 10, Appl
20	9	45.0	11	1	US-10-329-445-176	Sequence 176, App
21	9	45.0	12	1	US-10-450-797-1031	Sequence 1031, Ap
22	8.4	42.0	10	1	US-09-876-549-8	Sequence 8, Appl
C 23	8.4	42.0	10	1	US-09-263-959-926	Sequence 926, App
C 24	8.4	42.0	10	1	US-09-846-032B-138	Sequence 138, App
C 25	8.4	42.0	10	1	US-10-033-145-1554	Sequence 1554, Ap
26	8.4	42.0	10	1	US-10-006-069A-138	Sequence 138, App
C 27	8.4	42.0	10	1	US-10-330-627-830	Sequence 830, App
C 28	8.4	42.0	10	1	US-10-330-627-831	Sequence 831, App
C 29	8.4	42.0	10	1	US-10-314-669-130	Sequence 130, App
C 30	8.4	42.0	10	1	US-10-293-222-115	Sequence 115, App
C 31	8.4	42.0	11	1	US-10-669-861-130	Sequence 130, App
C 32	8.4	42.0	11	1	US-09-263-959-431	Sequence 431, App
C 33	8.4	42.0	11	1	US-09-249-155-234	Sequence 234, App
					US-10-001-670-15	Sequence 15, Appl

RESULT 1

```

US10-174-020-71
; Sequence 71, Application US/10174020
; Publication No. US20030232770A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULI
; FILE REFERENCE: RTS-0369
; CURRENT APPLICATION NUMBER: US/10/1
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ IDS NOS: 149

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ALIGNMENTS

Sequence 14,	Appli
Sequence 3,	Appli
Sequence 234,	Appli
Sequence 295,	Appli
Sequence 401,	Appli
Sequence 407,	Appli
Sequence 537,	Appli
Sequence 538,	Appli
Sequence 538,	Appli
Sequence 2056,	Appli
Sequence 2057,	Appli
Sequence 2334,	Appli
Sequence 2349,	Appli
Sequence 100,	Appli
Sequence 157,	Appli
Sequence 537,	Appli
Sequence 538,	Appli
Sequence 2056,	Appli
Sequence 2057,	Appli
Sequence 2334,	Appli
Sequence 2349,	Appli
Sequence 537,	Appli
Sequence 538,	Appli
Sequence 2056,	Appli
Sequence 2057,	Appli
Sequence 2334,	Appli
Sequence 2349,	Appli
Sequence 537,	Appli
Sequence 538,	Appli
Sequence 100,	Appli
Sequence 1659,	Appli
Sequence 1663,	Appli
Sequence 1659,	Appli
Sequence 1663,	Appli
Sequence 656,	Appli
Sequence 714,	Appli
Sequence 1007,	Appli
Sequence 51,	Appli
Sequence 118,	Appli
Sequence 33,	Appli
Sequence 52,	Appli
Sequence 1,	Appli
Sequence 1,	Appli
Sequence 1,	Appli
Sequence 47,	Appli
Sequence 1,	Appli

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:40:30 ; Search time 0.001 Seconds

(without alignments)
46.400 Million cell updates/sec

Title: US-09-436-060A-3

Perfect score: 20

Sequence: 1 cgttcctctctcgcgcct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 112 seqs, 1160 residues

Total number of hits satisfying chosen parameters: 224

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 112 summaries

Database : rni3.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	1	US-08-770-565-3
2	20	100.0	20	1	US-08-833-377-7
3	19	95.0	20	1	US-08-833-377-14
4	12	60.0	12	1	US-08-770-565-4
5	11	55.0	11	1	US-08-126-594-5
6	11	55.0	11	1	US-08-465-811A-5
7	11	55.0	11	1	US-08-619-542B-5
8	11	55.0	11	1	US-08-619-542B-48
9	11	55.0	12	1	US-08-126-594-6
10	11	55.0	12	1	US-08-465-811A-6
11	11	55.0	12	1	US-08-619-542B-6
12	11	55.0	14	1	US-08-294-424-33
13	9.4	47.0	11	1	US-08-173-489C-225
14	9.4	47.0	11	1	US-09-475-947A-95
15	9.4	47.0	12	1	US-08-242-664-3
16	9.4	47.0	12	1	US-08-242-664-6
17	9.4	47.0	12	1	US-08-484-138-3
18	9.4	47.0	12	1	US-08-484-138-6
19	9.4	47.0	12	1	US-08-367-069-9
20	9.4	47.0	12	1	US-08-173-489C-245
21	9.4	47.0	12	1	US-07-853-132A-10
22	9.4	47.0	12	1	US-09-835-370-62
23	9.4	47.0	12	1	US-08-126-594-22
24	9.4	47.0	12	1	US-08-484-138-3
25	9.4	47.0	12	1	US-08-484-138-6
26	9.4	47.0	12	1	US-08-367-069-9
27	9.4	47.0	12	1	US-08-173-489C-245
28	9.4	47.0	12	1	US-07-853-132A-10
29	9.4	47.0	12	1	US-09-835-370-62
30	9.4	47.0	12	1	US-08-126-594-22
31	9.4	47.0	12	1	US-08-484-138-3
32	9.4	47.0	12	1	US-08-484-138-6
33	9.4	47.0	12	1	US-08-367-069-9

9	45.0	10	1	US-09-508-753B-27	Sequence 27, Appl
9	45.0	10	1	US-09-884-363-10	Sequence 10, Appl
9	45.0	12	1	US-08-388-171-4	Sequence 4, Appl
9	45.0	12	1	US-08-388-171-6	Sequence 6, Appl
9	45.0	12	1	US-08-454-527-4	Sequence 4, Appl
9	45.0	12	1	US-08-454-527-6	Sequence 6, Appl
9	45.0	12	1	US-08-507-032-13	Sequence 13, Appl
9	45.0	12	1	5194376-13	Patent No. 5194376
8.4	42.0	10	1	US-08-173-489C-153	Sequence 153, App
8.4	42.0	10	1	US-08-173-489C-203	Sequence 203, App
8.4	42.0	10	1	US-08-585-888-19	Sequence 19, Appl
8.4	42.0	10	1	US-08-388-353-187	Sequence 187, App
8.4	42.0	10	1	US-08-488-551B-187	Sequence 187, App
8.4	42.0	10	1	US-08-522-384-54	Sequence 54, Appl
8.4	42.0	10	1	US-09-195-931-19	Sequence 19, Appl
8.4	42.0	11	1	US-08-671-824-8	Sequence 8, Appl
8.4	42.0	11	1	US-08-874-825-15	Sequence 15, Appl
8.4	42.0	11	1	US-08-663-824-15	Sequence 15, Appl
8.4	42.0	11	1	US-08-083-945C-8	Sequence 8, Appl
8.4	42.0	11	1	US-09-435-335-3	Sequence 3, Appl
8.4	42.0	11	1	US-09-231-303-15	Sequence 15, Appl
8.4	42.0	11	1	US-09-249-155A-234	Sequence 234, App
8.4	42.0	11	1	US-09-529-812A-5	Sequence 5, Appl
8.4	42.0	11	1	US-09-686-341-6	Sequence 6, Appl
8.4	42.0	11	1	PCT-US94-07107A-8	Sequence 8, Appl
8	40.0	8	1	US-08-859-954-262	Sequence 262, App
8	40.0	10	1	US-08-475-221B-48	Sequence 48, Appl
8	40.0	10	1	US-08-476-876-48	Sequence 48, Appl
8	40.0	10	1	US-08-465-590-137	Sequence 137, App
8	40.0	10	1	US-08-475-228A-656	Sequence 656, App
8	40.0	10	1	US-08-700-835B-3	Sequence 3, Appl
8	40.0	10	1	US-08-482-080A-656	Sequence 656, App
8	40.0	10	1	US-08-388-353-190	Sequence 190, App
8	40.0	10	1	US-08-488-551B-190	Sequence 190, App
8	40.0	10	1	US-08-522-384-11	Sequence 11, Appl
8	40.0	10	1	US-09-303-268-3	Sequence 3, Appl
8	40.0	10	1	US-08-711-417C-137	Sequence 137, App
8	40.0	10	1	US-09-116-049-5	Sequence 5, Appl
8	40.0	10	1	US-08-884-363-5	Sequence 5, Appl
8	40.0	10	1	US-08-884-363-5	Sequence 5, Appl
8	40.0	10	1	US-09-723-909-137	Sequence 137, App
8	40.0	10	1	US-09-579-536C-43	Sequence 43, Appl
8	40.0	10	1	PCT-US93-08743-137	Sequence 137, App
7.6	38.0	10	1	US-08-420-629-1	Sequence 1, Appl
7.4	37.0	9	1	US-08-331-398A-37	Sequence 37, Appl
7.4	37.0	9	1	US-08-331-397B-37	Sequence 37, Appl
7.4	37.0	9	1	US-08-759-804A-37	Sequence 37, Appl
7.4	37.0	9	1	US-08-461-607-17	Sequence 17, Appl
7.4	37.0	9	1	US-09-363-600-17	Sequence 17, Appl
7.4	37.0	9	1	US-09-227-693-37	Sequence 37, Appl
7.4	37.0	9	1	US-08-596-159-10	Sequence 10, Appl
7.4	37.0	9	1	US-09-328-925-40	Sequence 40, Appl
7.4	37.0	9	1	US-08-126-594-22	Sequence 22, Appl
7.4	37.0	9	1	US-08-485-811A-22	Sequence 22, Appl
7.4	37.0	9	1	US-08-509-858-3	Sequence 3, Appl
7.4	37.0	9	1	US-08-619-542B-22	Sequence 22, Appl
7.4	37.0	9	1	US-08-859-954-186	Sequence 186, App
7.4	37.0	9	1	US-08-859-954-187	Sequence 187, App
7.4	37.0	9	1	US-08-859-954-261	Sequence 261, App
7.4	37.0	9	1	US-08-859-954-309	Sequence 309, App
7.4	37.0	9	1	US-09-323-323-35	Sequence 35, Appl
7.4	37.0	9	1	US-09-594-108-35	Sequence 35, Appl
7.4	37.0	9	1	US-09-344-300-35	Sequence 35, Appl
7.4	37.0	9	1	US-08-091-569-12	Sequence 12, Appl
7.4	37.0	9	1	US-08-105-483-421	Sequence 421, Appl
7.4	37.0	9	1	US-08-185-232A-12	Sequence 12, Appl
7.4	37.0	9	1	US-08-234-573-4	Sequence 4, Appl
7.4	37.0	9	1	US-08-203-676-12	Sequence 12, Appl
7.4	37.0	9	1	US-08-416-523-12	Sequence 12, Appl
7.4	37.0	9	1	US-08-709-209-421	Sequence 421, App
7.4	37.0	9	1	US-08-303-275-129	Sequence 129, App
7.4	37.0	9	1	US-08-458-101-421	Sequence 421, App
7.4	37.0	9	1	US-08-465-590-126	Sequence 126, App

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:36:28 ; Search time 0.001 Seconds
(without alignments)
61.920 Million cell updates/sec

Title: US-09-436-060A-3

Perfect score: 20

Sequence: 1 cgttcctcttcctgcggcct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 135 seqs, 1548 residues

Total number of hits satisfying chosen parameters: 270

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 135 summaries

Database : rge3.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	20	100.0	20	1	ACCESSION: A84604
2	20	100.0	20	1	ACCESSION: AR063827
3	20	100.0	20	1	ACCESSION: AR079894
4	20	100.0	20	1	ACCESSION: BD023699
5	20	100.0	20	1	ACCESSION: BD059142
6	19	95.0	20	1	ACCESSION: A84597
7	19	95.0	20	1	ACCESSION: AR079898
8	19	95.0	20	1	ACCESSION: BD059138
9	12.8	64.0	17	1	ACCESSION: BD058138
10	12.8	64.0	17	1	ACCESSION: AX214616
11	12	60.0	12	1	ACCESSION: AX214617
12	12	60.0	12	1	ACCESSION: AR063828
13	11.8	59.0	15	1	ACCESSION: BD023700
14	11.4	57.0	14	1	ACCESSION: AX207455
15	11.4	57.0	14	1	ACCESSION: AX207455
16	11.4	57.0	14	1	ACCESSION: A89334
17	11	55.0	14	1	ACCESSION: BD201821
18	11	55.0	14	1	ACCESSION: BD066847
19	11	55.0	11	1	ACCESSION: AR051288
20	11	55.0	11	1	ACCESSION: AR051324
21	11	55.0	11	1	ACCESSION: AR051324
22	11	55.0	11	1	ACCESSION: I16936
23	11	55.0	11	1	ACCESSION: I16936
24	11	55.0	12	1	ACCESSION: I16937
25	11	55.0	12	1	ACCESSION: I16937
26	9.4	47.0	11	1	ACCESSION: AR036791
27	9.4	47.0	11	1	ACCESSION: AR030036
28	9.4	47.0	11	1	ACCESSION: Q832666
29	9.4	47.0	11	1	ACCESSION: Q835805
30	9.4	47.0	11	1	ACCESSION: Q837875
31	9.4	47.0	11	1	ACCESSION: AR241807
32	9.4	47.0	11	1	ACCESSION: AX471516
33	9.4	47.0	11	1	ACCESSION: AX626144
					ACCESSION: AX628454

C 34	9.4	47.0	11	1	AX628984
C 35	9.4	47.0	11	1	AX629631
C 36	9.4	47.0	12	1	AX629631
C 37	9.4	47.0	12	1	AX629631
C 38	9.4	47.0	12	1	AR030056
C 39	9.4	47.0	12	1	AR042879
C 40	9.4	47.0	12	1	AR175989
C 41	9.4	47.0	12	1	I28550
C 42	9.4	47.0	12	1	I28553
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C 78	9.4	47.0	12	1	I28553
C 79	9.4	47.0	12	1	I28553
C 80	9.4	47.0	12	1	I28553
C 81	9.4	47.0	12	1	I28553
C 82	9.4	47.0	12	1	I28553
C 83	9.4	47.0	12	1	I28553
C 84	9.4	47.0	12	1	I28553
C 85	9.4	47.0	12	1	I28553
C 86	9.4	47.0	12	1	I28553
C 87	9.4	47.0	12	1	I28553
C 88	9.4	47.0	12	1	I28553
C 89	9.4	47.0	12	1	I28553
C 90	9.4	47.0	12	1	I28553
C 91	9.4	47.0	12	1	I28553
C 92	9.4	47.0	12	1	I28553
C 93	9.4	47.0	12	1	I28553
C 94	9.4	47.0	12	1	I28553
C 95	9.4	47.0	12	1	I28553
C 96	9.4	47.0	12	1	I28553
C 97	9.4	47.0	12	1	I28553
C 98	9.4	47.0	12	1	I28553
C 99	9.4	47.0	12	1	I28553
C 100	9.4	47.0	12	1	I28553
C 101	9.4	47.0	12	1	I28553
C 102	9.4	47.0	12	1	I28553
C 103	9.4	47.0	12	1	I28553
C 104	9.4	47.0	12	1	I28553
C 105	9.4	47.0	12	1	I28553
C 106	9.4	47.0	12	1	I28553

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:52:39 ; Search time 0.001 Seconds
(without alignments)
17.760 Million cell updates/sec

Title: US-09-436-060A-4
Perfect score: 12
Sequence: 1 cgttcctcttcc 12

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 81 seqs, 740 residues

Total number of hits satisfying chosen parameters: 162

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 81 summaries

Database : rnpgb4.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	9	75.0	10	1	US-09-884-363-10
C 2	9	75.0	11	1	US-10-670-011-393
C 3	8.4	70.0	10	1	US-09-846-033B-138
C 4	8.4	70.0	10	1	US-10-006-069A-138
C 5	8.4	70.0	10	1	US-10-344-669-130
C 6	8.4	70.0	10	1	US-10-669-861-130
C 7	8.4	70.0	11	1	US-10-670-011-407
C 8	8	66.7	9	1	US-09-989-789-537
C 9	8	66.7	9	1	US-09-989-789-538
C 10	8	66.7	9	1	US-09-816-763-100
C 11	8	66.7	9	1	US-09-990-186-537
C 12	8	66.7	9	1	US-09-990-186-538
C 13	8	66.7	9	1	US-09-989-994-537
C 14	8	66.7	9	1	US-09-989-994-538
C 15	8	66.7	9	1	US-10-001-073-3
C 16	8	66.7	9	1	US-10-821-568-100
C 17	8	66.7	10	1	US-09-989-789-1659
C 18	8	66.7	10	1	US-09-989-789-1663
C 19	8	66.7	10	1	US-09-990-186-1659
C 20	8	66.7	10	1	US-09-990-186-1663
C 21	8	66.7	10	1	US-09-989-994-1659
C 22	8	66.7	10	1	US-09-989-994-1663
C 23	8	66.7	10	1	US-09-993-346-656
C 24	8	66.7	10	1	US-10-033-145-714
C 25	8	66.7	10	1	US-10-033-145-1007
C 26	8	66.7	10	1	US-10-055-713-47
C 27	8	66.7	10	1	US-10-055-711-51
C 28	8	66.7	10	1	US-10-418-552-33
C 29	8	66.7	10	1	US-10-650-454-52
C 30	8	66.7	10	1	US-10-470-180-47
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C 32	7.4	61.7	9	1	US-09-989-789-2035
C 33	7.4	61.7	9	1	US-09-989-789-2219

ALIGNMENTS

RESULT 1

US-09-884-363-10/c
; Sequence 10, Application US/09884363
; Publication No. US20030044392A1
; GENERAL INFORMATION:
; APPLICANT: Hung, Men-Chie
; TITLE OF INVENTION: HUMAN PEA3 IS A TUMOR SUPPRESSOR FOR CANCER CELLS
; FILE REFERENCE: UTSC:582
; CURRENT APPLICATION NUMBER: US/09/884,363
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/116,049
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Simian virus 40
US-09-884-363-10

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:51:03 : Search time 1 seconds
(without alignments)
0.017 Million cell updates/sec

Title: US-09-436-060A-4

Perfect score: 12

Sequence: 1 cgtctctcttc 12

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 83 seqs, 714 residues

Total number of hits satisfying chosen parameters: 166

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 83 summaries

Database : rni4.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	100.0	12	1	US-08-770-565-4
2	9	75.0	10	1	Sequence 4, Appli
3	9	75.0	10	1	Sequence 8, Appli
4	9	75.0	10	1	Sequence 8, Appli
5	9	75.0	10	1	Sequence 10, Appl
6	9	75.0	10	1	Sequence 27, Appl
7	9	75.0	10	1	Sequence 10, Appl
8	9	75.0	10	1	Sequence 13, Appl
9	8.4	70.0	10	1	Sequence 153, App
10	8.4	70.0	10	1	Sequence 203, App
11	8.4	70.0	11	1	Sequence 225, App
12	8	66.7	8	1	Sequence 262, App
13	8	66.7	10	1	Sequence 48, Appl
14	8	66.7	10	1	Sequence 48, Appl
15	8	66.7	10	1	Sequence 137, App
16	8	66.7	10	1	Sequence 656, App
17	8	66.7	10	1	Sequence 656, App
18	8	66.7	10	1	Sequence 188, App
19	8	66.7	10	1	Sequence 190, App
20	8	66.7	10	1	Sequence 188, App
21	8	66.7	10	1	Sequence 188, App
22	8	66.7	10	1	Sequence 190, App
23	8	66.7	10	1	Sequence 11, Appl
24	8	66.7	10	1	Sequence 137, App
25	8	66.7	10	1	Sequence 656, App
26	8	66.7	10	1	Sequence 16, Appl
27	8	66.7	10	1	Sequence 137, App
28	8	66.7	10	1	Sequence 137, App
29	7	58.3	7	1	Sequence 10, Appl
30	7	58.3	8	1	Sequence 187, App
31	7	58.3	8	1	Sequence 261, App
32	7	58.3	8	1	Sequence 309, App
33	7	58.3	9	1	Sequence 126, App

C 34	7	58.3	9	1	US-08-711-417C-126	Sequence 126, App
C 35	7	58.3	9	1	US-09-723-909-126	Sequence 126, App
C 36	7	58.3	9	1	PCT-US93-08743-126	Sequence 126, App
C 37	6.4	53.3	8	1	US-08-187-749-6	Sequence 2, Appli
C 38	6.4	53.3	8	1	US-08-662-963-2	Sequence 3, Appli
C 39	6.4	53.3	8	1	US-08-662-963-3	Sequence 3, Appli
C 40	6.4	53.3	8	1	US-08-662-963-10	Sequence 10, Appl
C 41	6.4	53.3	8	1	US-08-662-963-16	Sequence 16, Appl
C 42	6.4	53.3	8	1	US-08-662-963-18	Sequence 18, Appl
C 43	6.4	53.3	8	1	US-08-488-015B-15	Sequence 15, Appl
C 44	6.4	53.3	8	1	US-08-859-954-242	Sequence 242, App
C 45	6.4	53.3	8	1	US-08-859-954-551	Sequence 551, App
C 46	6.4	53.3	8	1	US-09-585-599A-3	Sequence 3, Appli
C 47	6.4	53.3	8	1	US-04-585-599A-5	Sequence 5, Appli
C 48	6.4	53.3	8	1	US-09-835-370-64	Sequence 64, Appl
C 49	6.4	53.3	8	1	PCT-US95-01104-6	Sequence 6, Appli
C 50	6.2	51.7	7	1	US-08-488-015B-21	Sequence 21, Appl
C 51	6	50.0	7	1	US-07-630-288A-9	Sequence 9, Appli
C 52	6	50.0	7	1	US-08-488-049-9	Sequence 9, Appli
C 53	6	50.0	7	1	US-08-855-372B-44	Sequence 44, Appl
C 54	6	50.0	7	1	US-08-855-372B-45	Sequence 45, Appl
C 55	6	50.0	7	1	US-08-855-372B-68	Sequence 68, Appl
C 56	6	50.0	7	1	US-08-855-372B-69	Sequence 69, Appl
C 57	6	50.0	7	1	US-09-498-851-44	Sequence 44, Appl
C 58	6	50.0	7	1	US-09-498-851-45	Sequence 45, Appl
C 59	6	50.0	7	1	US-09-498-851-68	Sequence 68, Appl
C 60	6	50.0	7	1	US-09-498-851-69	Sequence 69, Appl
C 61	6	50.0	7	1	US-09-328-925-2	Sequence 2, Appli
C 62	6	50.0	8	1	US-08-509-858-3	Sequence 3, Appli
C 63	6	50.0	8	1	US-08-465-590-135	Sequence 135, App
C 64	6	50.0	8	1	US-08-227-180B-4	Sequence 4, Appli
C 65	6	50.0	8	1	US-08-227-180B-5	Sequence 5, Appli
C 66	6	50.0	8	1	US-08-859-954-129	Sequence 129, App
C 67	6	50.0	8	1	US-08-859-954-186	Sequence 186, App
C 68	6	50.0	8	1	US-08-859-954-263	Sequence 263, App
C 69	6	50.0	8	1	US-08-859-954-264	Sequence 264, App
C 70	6	50.0	8	1	US-08-859-954-291	Sequence 291, App
C 71	6	50.0	8	1	US-08-859-954-354	Sequence 354, App
C 72	6	50.0	8	1	US-08-859-954-434	Sequence 434, App
C 73	6	50.0	8	1	US-08-859-954-482	Sequence 482, App
C 74	6	50.0	8	1	US-08-859-954-483	Sequence 483, App
C 75	6	50.0	8	1	US-08-859-954-518	Sequence 518, App
C 76	6	50.0	8	1	US-08-859-954-559	Sequence 559, App
C 77	6	50.0	8	1	US-08-859-954-559	Sequence 559, App
C 78	6	50.0	8	1	US-08-711-417C-135	Sequence 135, App
C 79	6	50.0	8	1	US-09-723-909-135	Sequence 135, App
C 80	6	50.0	8	1	US-09-682-562-1	Sequence 1, Appli
C 81	6	50.0	8	1	US-09-682-562-3	Sequence 3, Appli
C 82	6	50.0	8	1	PCT-US93-08743-135	Sequence 135, App
C 83	6	50.0	8	1		

ALIGNMENTS

RESULT 1
US-08-770-565-4
Sequence 4, Application US/0870565
Patent No. 5846723

GENERAL INFORMATION:

APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:49:39 ; Search time 1 Seconds

(without alignments)
0.038 Million cell updates/sec

Title: US-09-436-060A-4

Perfect score: 12

Sequence: 1 cgtctctcttc 12

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 160 seqs, 1603 residues

Total number of hits satisfying chosen parameters: 320

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 160 summaries

Database : rng4.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	10	83.3	12	1 AB117803	Oligonucleotide pr
4	10	83.3	12	1 AC622980	Tandem N-box probe
5	10	83.3	12	1 ADA00988	Mouse DNA containi
6	10	83.3	12	1 AD010236	GA binding protein
7	9.4	78.3	11	1 ABV68239	Human skin EST 602
8	9.4	78.3	11	1 ADQ32773	Human hair-bearing
9	9.4	78.3	11	1 ADQ35220	Human facial skin-
10	9.4	78.3	12	1 AB128525	Oligonucleotide pr
11	9.4	78.3	12	1 AB123385	Oligonucleotide pr
12	9.4	78.3	12	1 AB103041	Oligonucleotide pr
13	9.4	78.3	12	1 AB128526	Oligonucleotide pr
14	9.4	78.3	12	1 ABH69570	Oligonucleotide pr
15	9	75.0	10	1 AA250022	SV40 enhancer for
16	9	75.0	10	1 AAF43218	Yeast NORF gene SA
17	9	75.0	12	1 AAX37031	NF-AT complex bind
18	9	75.0	12	1 AAX54574	Human IGE receptor
19	9	75.0	12	1 ABF21434	Human IGE receptor
20	9	75.0	12	1 ABF3924	Oligonucleotide pr
21	9	75.0	12	1 AB111122	Oligonucleotide pr
22	9	75.0	12	1 ABH80463	Oligonucleotide pr
23	9	75.0	12	1 ABH86427	Oligonucleotide pr
24	9	75.0	12	1 AB177320	Oligonucleotide pr
25	9	75.0	12	1 AB124917	Oligonucleotide pr
26	9	75.0	12	1 ABH74926	Oligonucleotide pr
27	9	75.0	12	1 ABH7651	Oligonucleotide pr
28	9	75.0	12	1 ABH70318	Oligonucleotide pr
29	9	75.0	12	1 AB166296	Oligonucleotide pr
30	9	75.0	12	1 AB166297	Oligonucleotide pr
31	9	75.0	12	1 AB161631	Oligonucleotide pr
32	9	75.0	12	1 AB148099	Oligonucleotide pr
33	9	75.0	12	1 ABH88407	Oligonucleotide pr

C 34	9	75.0	12	1 ABI50506	Oligonucleotide pr
35	9	75.0	12	1 ABZ37128	Human IGE receptor
36	9	75.0	12	1 ABD19038	Human IGE receptor
37	8.4	70.0	10	1 AAX14816	Triple helix formi
38	8.4	70.0	10	1 AAX14766	Triple helix formi
39	8.4	70.0	10	1 AAZ81034	Metastatic breast
40	8.4	70.0	10	1 AAZ83081	Metastatic breast
41	8.4	70.0	10	1 AAZ86177	Metastatic breast
42	8.4	70.0	10	1 AAF35028	Yeast NORF gene SA
43	8.4	70.0	10	1 AAF38850	Yeast NORF gene SA
44	8.4	70.0	10	1 AAF40144	Yeast NORF gene SA
45	8.4	70.0	10	1 AAF41776	Yeast NORF gene SA
46	8.4	70.0	10	1 AAF37562	Yeast NORF gene SA
47	8.4	70.0	10	1 AAD32508	Human VEGF zinc fi
48	8.4	70.0	10	1 ABT04103	Human VEGF zinc fi
49	8.4	70.0	10	1 ABL91869	Human LIPG Gene pr
50	8.4	70.0	10	1 ABL45773	Human MMP13 gene a
51	8.4	70.0	10	1 ACD06060	Human VEGF-targete
52	8.4	70.0	10	1 ACD19282	Human VEGF-targete
53	8.4	70.0	10	1 ADG98629	Human CERP gene al
54	8.4	70.0	10	1 ADL33591	DNA binding protei
55	8.4	70.0	10	1 ADM72632	DNA sequence of tar
56	8.4	70.0	11	1 AAX14838	Triple helix formi
57	8.4	70.0	11	1 ABV67129	Human skin EST 491
58	8.4	70.0	11	1 ABV67709	Human skin EST 549
59	8.4	70.0	11	1 ABV62872	Human skin EST 658
60	8.4	70.0	11	1 ABV62855	Human skin EST 405
61	8.4	70.0	11	1 ABV70293	Human skin EST 807
62	8.4	70.0	11	1 ADQ34843	Human facial skin-
63	8	66.7	8	1 AAB80949	A. thaliana primer
64	8	66.7	9	1 ABQ71419	Zinc finger protei
65	8	66.7	9	1 ABQ71418	Zinc finger protei
66	8	66.7	9	1 ADA62567	Zinc finger target
67	8	66.7	9	1 ADA62566	Zinc finger target
68	8	66.7	9	1 ADM30770	Synthetic zinc fin
69	8	66.7	9	1 ADM30771	Synthetic zinc fin
70	8	66.7	10	1 AQG61538	IL2 PuBp enhancer
71	8	66.7	10	1 AAQ96592	HIV-1 NL4-3 nef ge
72	8	66.7	10	1 AAQ96593	HIV-1 NL4-3 nef ge
73	8	66.7	10	1 AAQ96594	HIV-1 NL4-3 nef ge
74	8	66.7	10	1 AAT93280	5'-primer for mam
75	8	66.7	10	1 AAV45395	PuBp binding site
76	8	66.7	10	1 AAV67094	IL2 enhancer PuBp
77	8	66.7	10	1 AAV50139	Yeast tag for NORF
78	8	66.7	10	1 AAX17656	PNA-thiazole orang
79	8	66.7	10	1 AAX17656	Bis-distamycin tar
80	8	66.7	10	1 AAZ78579	Human dendritic ce
81	8	66.7	10	1 AAZ78286	Human dendritic ce
82	8	66.7	10	1 AAZ81452	Metastatic breast
83	8	66.7	10	1 AAZ84987	Metastatic breast
84	8	66.7	10	1 AAZ83001	Metastatic breast
85	8	66.7	10	1 AAF33370	Yeast NORF gene SA
86	8	66.7	10	1 AAF33640	Yeast NORF gene SA
87	8	66.7	10	1 AAF33356	Yeast NORF gene SA
88	8	66.7	10	1 AAF3381	Yeast NORF gene SA
89	8	66.7	10	1 AAF34913	Yeast NORF gene SA
90	8	66.7	10	1 AAF39588	Yeast NORF gene SA
91	8	66.7	10	1 ABK68703	Human SCY2 Gene a
92	8	66.7	10	1 ABK95861	Solute Carrier Fam
93	8	66.7	10	1 ABK83147	DNA binding molecu
94	8	66.7	10	1 ABL52311	Human CCR6 prefer
95	8	66.7	10	1 ABQ71667	Zinc finger protei
96	8	66.7	10	1 ABQ71671	Zinc finger protei
97	8	66.7	10	1 AAD43427	Human CYP3A5 gene
98	8	66.7	10	1 AAL40868	Zinc finger protei
99	8	66.7	10	1 AAL41867	Human GONT1 allele
100	8	66.7	10	1 ABH85907	Gamma tocopherol m
101	8	66.7	10	1 ABT14371	Nucleic acid PCR a
102	8	66.7	10	1 ADA63692	Zinc finger target
103	8	66.7	10	1 ADA63688	Zinc finger target
104	8	66.7	10	1 ADJ78763	Arabidopsis gamma-
105	8	66.7	10	1 ADM22190	Synthetic zinc fin
106	8	66.7	10	1 ADM22186	Synthetic zinc fin

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:47:56 ; Search time 0.001 Seconds
(without alignments)
15.144 Million cell updates/sec

Title: US-09-436-060A-4

Perfect score: 12

Sequence: 1 cgtctctcttc 12

Scoring table: IDENTITY NUC

Gapop 10.0 , Capext 0.5

Searched: 65 seqs, 631 residues

Total number of hits satisfying chosen parameters: 130

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : rge4.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	100.0	12	1	AR063828
2	12	100.0	12	1	BD023700
3	9.4	78.3	11	1	AR063828
4	9.4	78.3	11	1	AR063828
5	9.4	78.3	11	1	AR063828
6	9.4	78.3	11	1	AR063828
7	9.4	78.3	11	1	AR063828
8	9.4	78.3	11	1	AR063828
9	9.4	78.3	11	1	AR063828
10	9.4	78.3	11	1	AR063828
11	9.4	78.3	11	1	AR063828
12	9.4	78.3	11	1	AR063828
13	9.4	78.3	11	1	AR063828
14	9.4	78.3	11	1	AR063828
15	9.4	78.3	11	1	AR063828
16	9.4	78.3	11	1	AR063828
17	9.4	78.3	11	1	AR063828
18	9.4	78.3	11	1	AR063828
19	9.4	78.3	11	1	AR063828
20	9.4	78.3	11	1	AR063828
21	9.4	78.3	11	1	AR063828
22	9.4	78.3	11	1	AR063828
23	9.4	78.3	11	1	AR063828
24	9.4	78.3	11	1	AR063828
25	9.4	78.3	11	1	AR063828
26	9.4	78.3	11	1	AR063828
27	9.4	78.3	11	1	AR063828
28	9.4	78.3	11	1	AR063828
29	9.4	78.3	11	1	AR063828
30	9.4	78.3	11	1	AR063828
31	9.4	78.3	11	1	AR063828
32	9.4	78.3	11	1	AR063828
33	9.4	78.3	11	1	AR063828

34	8	66.7	10	1	AR209708
35	8	66.7	10	1	AR236019
36	8	66.7	10	1	AR351850
37	8	66.7	10	1	AR351854
38	8	66.7	10	1	AR404849
39	8	66.7	10	1	AR668210
40	8	66.7	10	1	AR668214
41	8	66.7	10	1	BD065159
42	7.4	61.7	9	1	AR667139
43	7.4	61.7	9	1	AR668586
44	7.4	61.7	9	1	AR668770
45	7.4	61.7	9	1	AR668831
46	7.4	61.7	9	1	AR668978
47	7.4	61.7	9	1	AR668979
48	7.4	61.7	9	1	AR668980
49	7.4	61.7	9	1	AR669025
50	7.4	61.7	9	1	AR669062
51	7.4	61.7	9	1	AR669084
52	7.4	61.7	9	1	AR669085
53	7.4	61.7	9	1	AR669086
54	7.4	61.7	9	1	AR669087
55	6.4	53.3	8	1	AR669088
56	6.4	53.3	8	1	AR669089
57	6.4	53.3	8	1	AR669090
58	6.4	53.3	8	1	AR669091
59	6.4	53.3	8	1	AR669092
60	6.4	53.3	8	1	AR669093
61	6.4	53.3	8	1	AR669094
62	6.4	53.3	8	1	AR669095
63	6.4	53.3	8	1	AR669096
64	6.4	53.3	8	1	AR669097
65	6.4	53.3	8	1	AR669098

ALIGNMENTS

RESULT 1	AR063828	12 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	Sequence 4 from patent US 5846723.				
DEFINITION	AR063828				
ACCESSION	AR063828				
VERSION	AR063828.1				
KEYWORDS	GI:5993136				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 12)				
AUTHORS	Kim N.Woo., Wu, F., Kealey, J.T., Pruzan, R. and Weinrich, S.L.				
TITLE	Methods for detecting the RNA component of telomerase				
JOURNAL	Patent: US 5846723-A 08-DEC-1998;				
FEATURES	Location/Qualifiers				
source	1..12				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	100.0%; Score 12; DB 1; Length 12;				
Best Local Similarity	100.0%; Pred. No. 3.1;				
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1 CGTCTCTCTTC 12				
	1 CGTCTCTCTTC 12				
Db					
RESULT 2	BD023700	12 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	Method for detecting and inhibiting RNA component of telomerase.				
DEFINITION	BD023700				
ACCESSION	BD023700.1				
VERSION	GI:22564923				
KEYWORDS	JP 2001507229-A/4.				
SOURCE	unidentified				

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 09:03:59 ; Search time 1 Seconds
(without alignments)
0.014 Million cell updates/sec

Title: US-09-436-060A-6
Perfect score: 20
Sequence: 1 ctgacagagcccaactcttc 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 36 seqs, 361 residues

Total number of hits satisfying chosen parameters: 72

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 36 summaries

Database : rnpb6.seq:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.4	72.0	19	1	US-10-093-958-22
2	9	45.0	10	1	US-10-033-145-87
3	9	45.0	10	1	US-10-033-145-87
4	9	45.0	10	1	US-10-033-145-87
5	8.4	42.0	10	1	US-03-154-750A-53
6	8.4	42.0	10	1	US-03-989-789-1273
7	8.4	42.0	10	1	US-03-990-186-1273
8	8.4	42.0	10	1	US-03-990-186-1273
9	8.4	42.0	10	1	US-03-990-186-1273
10	8.4	42.0	10	1	US-03-990-186-1273
11	8.4	42.0	10	1	US-03-990-186-1273
12	8.4	42.0	10	1	US-03-990-186-1273
13	8.4	42.0	10	1	US-03-990-186-1273
14	8.4	42.0	10	1	US-03-990-186-1273
15	8.4	42.0	10	1	US-03-990-186-1273
16	8.4	42.0	10	1	US-03-990-186-1273
17	8.4	42.0	10	1	US-03-990-186-1273
18	8.4	42.0	10	1	US-03-990-186-1273
19	8.4	42.0	10	1	US-03-990-186-1273
20	8.4	42.0	10	1	US-03-990-186-1273
21	8.4	42.0	10	1	US-03-990-186-1273
22	8.4	42.0	10	1	US-03-990-186-1273
23	8.4	42.0	10	1	US-03-990-186-1273
24	8.4	42.0	10	1	US-03-990-186-1273
25	8.4	42.0	10	1	US-03-990-186-1273
26	7.4	37.0	9	1	US-03-989-789-2433
27	7.4	37.0	9	1	US-03-989-789-2433
28	7.4	37.0	9	1	US-03-989-789-2433
29	7.4	37.0	9	1	US-03-989-789-2433
30	7.4	37.0	9	1	US-03-989-789-2433
31	7.4	37.0	9	1	US-03-989-789-2433
32	7.4	37.0	9	1	US-03-989-789-2433
33	7.4	37.0	9	1	US-03-989-789-2433

ALIGNMENTS

RESULT 1

US-10-093-958-22
; Sequence 22, Application US/10093958
; Publication No. US20030044423A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Jeffrey, Way
; TITLE OF INVENTION: Expression Technology for Proteins Containing a Hybrid Isotype An
; FILE REFERENCE: MOIETY
; CURRENT APPLICATION NUMBER: US/10/093,958
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,096
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 22
; LENGTH: 19
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: forward primer for gamma 1 hinge region
US-10-093-958-22

Query Match 72.0%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGAGCCCAACTCTTC 20
DB 4 CAGAGCCCAACTCTTC 19

RESULT 2

US-10-033-145-87/c
; Sequence 87, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 87
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-87

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGAGCCCA 13
DB 9 CAGAGCCCA 1

RESULT 3

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 09:01:36 ; Search time 0.001 Seconds
(without alignments)
8.400 Million cell updates/sec

Title: US-09-436-060A-6

Perfect score: 20

Sequence: .. 1 ctgacagagcccaactcttc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 21 seqs, 210 residues

Total number of hits satisfying chosen parameters: 42

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 21 summaries

Database : rni6.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	20	100.0	20	1	US-08-770-565-6
2	12.4	62.0	15	1	US-08-311-486C-658
3	9	45.0	12	1	US-09-508-753B-472
4	8.4	42.0	10	1	US-08-388-353-191
5	8.4	42.0	10	1	US-08-388-353-192
6	8.4	42.0	10	1	US-08-488-551B-191
7	8.4	42.0	10	1	US-08-488-551B-192
8	8.4	42.0	10	1	US-09-154-750A-53
9	8.4	42.0	11	1	US-09-249-155A-220
10	8	40.0	8	1	US-08-859-954-300
11	8	40.0	10	1	US-08-171-718-21
12	8	40.0	10	1	US-08-478-087-21
13	7.4	37.0	9	1	PCT-US91-03680-137
14	7	35.0	8	1	US-08-859-954-224
15	7	35.0	8	1	US-08-859-954-226
16	7	35.0	8	1	US-08-859-954-281
17	7	35.0	8	1	US-08-859-954-458
18	7	35.0	8	1	US-08-859-954-463
19	7	35.0	8	1	US-09-063-450-4
20	7	35.0	8	1	US-09-781-697-3
21	6.8	34.0	9	1	PCT-US91-03680-139

ALIGNMENTS

RESULT 1
US-08-770-565-6
; Sequence 6, Application US/0870565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred

APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-6

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCACTCTTC 20
Db 1 CTGACAGAGCCCACTCTTC 20

RESULT 2
US-08-311-486C-658
; Sequence 658, Application US/08311486C
; Patent No. 5811300
; GENERAL INFORMATION:
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth Draper
; APPLICANT: Kevin Kisich
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: TNF-
NUMBER OF SEQUENCES: 1157
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2086
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage

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3702 DNA 20 bp

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 09:12:29 ; Search time 0.001 Seconds

(without alignments)
64.160 Million cell updates/sec

Title: US-09-436-060A-7

Perfect score: 20

Sequence: 1 ccaactcttcgctggcag 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 0.5

Searched: 147 seqs, 1604 residues

Total number of hits satisfying chosen parameters: 294

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 147 summaries

Database : rng7.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	1 AAV41174	RNA component of h
2	16	80.0	21	1 ADF93861	Human TERT siRNA,
3	16	80.0	21	1 ADG30030	hTR-targeted siNA
4	11	55.0	12	1 AB141062	Oligonucleotide pr
5	11	55.0	13	1 AAX00290	Target DNA sequenc
6	10.4	52.0	12	1 AB119475	Oligonucleotide pr
7	10.4	52.0	13	1 AAX00297	Target DNA sequenc
8	10.4	52.0	13	1 ABC70351	Oligonucleotide SE
9	10.4	52.0	13	1 ABE97741	Oligonucleotide SE
10	10.4	52.0	13	1 ABE97741	Oligonucleotide SE
11	10.4	52.0	13	1 ABE97741	Oligonucleotide SE
12	10	50.0	10	1 ABF40580	Oligonucleotide SE
13	10	50.0	12	1 ABF40580	Oligonucleotide SE
14	10	50.0	12	1 ABF40580	Oligonucleotide SE
15	10	50.0	12	1 ABF40580	Oligonucleotide SE
16	10	50.0	12	1 ABF40580	Oligonucleotide SE
17	10	50.0	13	1 ABF40580	Oligonucleotide SE
18	10	50.0	13	1 ABF40580	Oligonucleotide SE
19	10	50.0	13	1 ABF40580	Oligonucleotide SE
20	10	50.0	13	1 ABF40580	Oligonucleotide SE
21	10	50.0	13	1 ABF40580	Oligonucleotide SE
22	9.4	47.0	11	1 ABF40580	Oligonucleotide SE
23	9.4	47.0	11	1 ABF40580	Oligonucleotide SE
24	9.4	47.0	11	1 ABF40580	Oligonucleotide SE
25	9.4	47.0	11	1 ABF40580	Oligonucleotide SE
26	9.4	47.0	11	1 ABF40580	Oligonucleotide SE
27	9.4	47.0	11	1 ABF40580	Oligonucleotide SE
28	9.4	47.0	11	1 ABF40580	Oligonucleotide SE
29	9	45.0	10	1 AAV50086	Yeast tag for puta
30	9	45.0	10	1 AAV50086	Metastatic breast
31	9	45.0	10	1 AAV50086	Yeast putative cod
32	9	45.0	10	1 AAV50086	Yeast NORF gene SA
33	9	45.0	10	1 AAV50086	Yeast NORF gene SA

34	9	45.0	10	1 AAF34145	Yeast NORF gene SA
35	9	45.0	10	1 AAF34145	Human allergenic dis
36	9	45.0	11	1 AAD32705	pWB plasmid DNA ha
37	9	45.0	12	1 ABH67877	Oligonucleotide pr
38	9	45.0	12	1 ABH67877	Oligonucleotide pr
39	9	45.0	12	1 ABH67877	Oligonucleotide pr
40	9	45.0	12	1 ABH67877	Oligonucleotide pr
41	9	45.0	12	1 ABH67877	Oligonucleotide pr
42	9	45.0	12	1 ABH67877	Oligonucleotide pr
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44	9	45.0	12	1 ABH67877	Oligonucleotide pr
45	9	45.0	12	1 ABH67877	Oligonucleotide pr
46	9	45.0	12	1 ABH67877	Oligonucleotide pr
47	9	45.0	12	1 ABH67877	Oligonucleotide pr
48	9	45.0	12	1 ABH67877	Oligonucleotide pr
49	9	45.0	12	1 ABH67877	Oligonucleotide pr
50	9	45.0	12	1 ABH67877	Oligonucleotide pr
51	9	45.0	12	1 ABH67877	Oligonucleotide pr
52	9	45.0	12	1 ABH67877	Oligonucleotide pr
53	9	45.0	12	1 ABH67877	Oligonucleotide pr
54	9	45.0	12	1 ABH67877	Oligonucleotide pr
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56	9	45.0	12	1 ABH67877	Oligonucleotide pr
57	9	45.0	12	1 ABH67877	Oligonucleotide pr
58	8.4	42.0	10	1 AAV50303	HIV-1 NL4-3 nef ge
59	8.4	42.0	10	1 AAV50303	Yeast tag for addi
60	8.4	42.0	10	1 AAV50303	Metastatic breast
61	8.4	42.0	10	1 AAV50303	Metastatic breast
62	8.4	42.0	10	1 AAV50303	Metastatic breast
63	8.4	42.0	10	1 AAV50303	Metastatic breast
64	8.4	42.0	10	1 AAV50303	Metastatic breast
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67	8.4	42.0	10	1 AAV50303	Human ubiquitously
68	8.4	42.0	10	1 AAV50303	Human normal hepat
69	8.4	42.0	10	1 AAV50303	Yeast NORF gene SA
70	8.4	42.0	10	1 AAV50303	Yeast NORF gene SA
71	8.4	42.0	10	1 AAV50303	Yeast NORF gene SA
72	8.4	42.0	10	1 AAV50303	Yeast NORF gene SA
73	8.4	42.0	10	1 AAV50303	Human CHRE gene p
74	8.4	42.0	10	1 AAV50303	Solute Carrier Fam
75	8.4	42.0	10	1 AAV50303	Human HTATIP PCR p
76	8.4	42.0	10	1 AAV50303	Human LIFE gene po
77	8.4	42.0	10	1 AAV50303	Human ORG1 gene p
78	8.4	42.0	10	1 AAV50303	Human CSF3 gene al
79	8.4	42.0	10	1 AAV50303	Zinc finger protei
80	8.4	42.0	10	1 AAV50303	Zinc finger protei
81	8.4	42.0	10	1 AAV50303	Human homeo box D3
82	8.4	42.0	10	1 AAV50303	Human testis-ehan
83	8.4	42.0	10	1 AAV50303	Human testis-ehan
84	8.4	42.0	10	1 AAV50303	DNA tag from human
85	8.4	42.0	10	1 AAV50303	TIT-5 SAGE tag nuc
86	8.4	42.0	10	1 AAV50303	TIT-5 SAGE tag, H
87	8.4	42.0	10	1 AAV50303	APBS12 primer used
88	8.4	42.0	10	1 AAV50303	Zinc finger target
89	8.4	42.0	10	1 AAV50303	Zinc finger target
90	8.4	42.0	10	1 AAV50303	Synthetic zinc fin
91	8.4	42.0	10	1 AAV50303	Synthetic zinc fin
92	8.4	42.0	10	1 AAV50303	CD15+ myeloid cell
93	8.4	42.0	11	1 AAV50303	Human skin stress/
94	8.4	42.0	11	1 AAV50303	Human skin EST 546
95	8.4	42.0	11	1 AAV50303	Human skin EST 552
96	8.4	42.0	11	1 AAV50303	Human skin EST 369
97	8.4	42.0	11	1 AAV50303	Human hair-bearing
98	8.4	42.0	11	1 AAV50303	Human facial skin-
99	8	40.0	9	1 AAV50303	Zinc finger protei
100	8	40.0	9	1 AAV50303	Zinc finger protei
101	8	40.0	9	1 AAV50303	Zinc finger target
102	8	40.0	9	1 AAV50303	Zinc finger target
103	8	40.0	9	1 AAV50303	Synthetic zinc fin
104	8	40.0	9	1 AAV50303	Synthetic zinc fin
105	8	40.0	9	1 AAV50303	Human EGFR small i
106	8	40.0	10	1 AAV50303	Probe used in DNA

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 09:11:16 / Search time 0.001 Seconds
(without alignments)
25.360 Million cell updates/sec

Title: US-09-436-060A-7

Perfect score: 20

Sequence: 1 ccaactcttcgcggtggcag 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 0.5

Searched: 60 seqs, 634 residues

Total number of hits satisfying chosen parameters: 120

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database: rge7.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	1	AR063831
2	20	100.0	20	1	BD023703
C 3	10.8	54.0	14	1	AR9176
C 4	10.8	54.0	14	1	BD066689
C 5	10	50.0	11	1	118772
C 6	10	50.0	11	1	195608
7	9.4	47.0	11	1	AX629495
8	9	45.0	10	1	BD065106
C 9	8.4	42.0	10	1	BD168118
C 10	8.4	42.0	10	1	ES4735
11	8.4	42.0	10	1	AR351835
12	8.4	42.0	10	1	AR351836
C 13	8.4	42.0	10	1	AX152445
C 14	8.4	42.0	10	1	AX377146
15	8.4	42.0	10	1	AX668192
16	8.4	42.0	10	1	AX668191
C 17	8.4	42.0	10	1	AX814791
C 18	8.4	42.0	10	1	BD065323
C 19	8.4	42.0	10	1	BD167133
C 20	8.4	42.0	10	1	BD167245
21	8.4	42.0	11	1	CQ833209
C 22	8.4	42.0	11	1	CQ836219
C 23	8.4	42.0	11	1	AX471580
C 24	8.4	42.0	11	1	AX626651
C 25	8.4	42.0	11	1	AX628423
C 26	8.4	42.0	11	1	AX628485
27	8.4	42.0	11	1	AX629184
28	8	40.0	9	1	AX668855
29	8	40.0	9	1	AX668856
30	8	40.0	10	1	AR026407
31	8	40.0	10	1	AR052583
C 32	8	40.0	10	1	BD238745
33	8	40.0	10	1	BD238911

C 34	8	40.0	10	1	E39527
C 35	8	40.0	10	1	E39571
C 36	8	40.0	10	1	I34894
37	8	40.0	10	1	I83515
38	8	40.0	10	1	AR351805
39	8	40.0	10	1	AR351839
40	8	40.0	10	1	AR351855
41	8	40.0	10	1	AR351863
42	8	40.0	10	1	AR351866
43	8	40.0	10	1	AR351883
44	8	40.0	10	1	AR351884
45	8	40.0	10	1	AR473558
46	8	40.0	10	1	AX214428
47	8	40.0	10	1	AX320713
48	8	40.0	10	1	AX668156
49	8	40.0	10	1	AX668195
50	8	40.0	10	1	AX668215
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52	8	40.0	10	1	AX668226
53	8	40.0	10	1	AX668243
54	8	40.0	10	1	AX668244
C 55	8	40.0	10	1	BD007856
C 56	8	40.0	10	1	BD083291
57	8	40.0	10	1	BD166512
C 58	8	40.0	10	1	S75141
C 59	7.4	37.0	9	1	AX665471
C 60	7.4	37.0	9	1	BD069703

ALIGNMENTS

RESULT 1	AR063831	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR063831	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
DEFINITION	AR063831	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
ACCESSION	AR063831	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
VERSION	AR063831.1	GI:5993139	20 bp	DNA	linear	PAT 29-SEP-1999
KEYWORDS	AR063831.1	GI:5993139	20 bp	DNA	linear	PAT 29-SEP-1999
SOURCE	Unknown.	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
ORGANISM	Unknown.	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
REFERENCE	1 (bases 1 to 20)	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
AUTHORS	Kim, N.W., Wu, F., Kealey, J.T., Pruzan, R. and Weinrich, S.L.	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
TITLE	Methods for detecting the RNA component of telomerase	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
JOURNAL	Patent: US 5846723-A 7 08-DEC-1998	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
FEATURES	Location/Qualifiers	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
source	1..20	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
	/organism="unknown"	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999
	/mol_type="unassigned DNA"	Sequence 7 from patent US 5846723.	20 bp	DNA	linear	PAT 29-SEP-1999

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CCAACTCTTCGCGGTGGCAG 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CCAACTCTTCGCGGTGGCAG 20

RESULT 2	BD023703	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD023703	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002
DEFINITION	BD023703	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002
ACCESSION	BD023703	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002
VERSION	BD023703.1	GI:22564926	20 bp	DNA	linear	PAT 27-AUG-2002
KEYWORDS	JP 2001507229-A/7.	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002
SOURCE	unidentified	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002
ORGANISM	unclassified.	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002
REFERENCE	1 (bases 1 to 20)	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002
AUTHORS	Kim, N.W., Wu, F., Kealey, J.T., Pruzan, R. and Weinrich, S.L.	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002
TITLE	Method for detecting and inhibiting RNA component of telomerase	Method for detecting and inhibiting RNA component of telomerase.	20 bp	DNA	linear	PAT 27-AUG-2002

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 09:14:02 ; Search time 0.001 Seconds
(without alignments)
8.960 Million cell updates/sec

Title: US-09-436-060A-7
Perfect score: 20
Sequence: 1 ccaactcttcggtgagcag 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5
Searched: 22 seqs, 224 residues

Total number of hits satisfying chosen parameters: 44
Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 22 summaries

Database : rni7.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	1 US-08-770-565-7	Sequence 7, Appl
C 2	10	50.0	11	1 US-07-778-233B-3	Sequence 3, Appl
C 3	10	50.0	11	1 US-07-963-321-3	Sequence 3, Appl
C 4	10	50.0	11	1 US-08-290-641-3	Sequence 3, Appl
C 5	10	50.0	11	1 US-08-548-540-3	Sequence 3, Appl
C 6	10	50.0	11	1 PCT-US96-09809-3	Sequence 3, Appl
C 7	8.4	42.0	10	1 US-08-388-353-191	Sequence 191, App
C 8	8.4	42.0	10	1 US-08-488-551B-191	Sequence 191, App
C 9	8	40.0	10	1 US-08-410-116B-21	Sequence 21, Appl
C 10	8	40.0	10	1 US-08-667-689A-21	Sequence 21, Appl
C 11	8	40.0	10	1 US-08-712-011-21	Sequence 21, Appl
C 12	8	40.0	10	1 US-08-478-239A-21	Sequence 21, Appl
C 13	8	40.0	10	1 US-09-779-233-36	Sequence 36, Appl
C 14	7.4	37.0	9	1 US-08-850-347-3	Sequence 3, Appl
C 15	7.4	37.0	9	1 US-08-990-065-3	Sequence 3, Appl
C 16	7.4	37.0	9	1 US-09-380-532-10	Sequence 10, Appl
C 17	7.4	37.0	9	1 PCT-US91-03680-137	Sequence 137, App
C 18	7	35.0	8	1 US-09-398-499-22	Sequence 22, Appl
C 19	7	35.0	8	1 US-09-398-499-45	Sequence 45, Appl
C 20	7	35.0	9	1 US-08-798-738-3	Sequence 3, Appl
C 21	7	35.0	9	1 US-10-096-596-33	Sequence 33, Appl
C 22	6.8	34.0	9	1 PCT-US91-03680-139	Sequence 139, App

ALIGNMENTS

RESULT 1
US-08-770-565-7
; Sequence 7, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo

APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-7
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.073; 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAACTCTTCGCGTGGCAG 20
DB 1 CCAACTCTTCGCGTGGCAG 20
RESULT 2
US-07-778-233B-3/c
; Sequence 3, Application US/07778233B
; Patent No. 5270170
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/778,233B
FILING DATE: 19911016

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 09:37:16 ; Search time 0.001 Seconds
(without alignments)
15.618 Million cell updates/sec

Title: US-09-436-060A-9
Perfect score: 19
Sequence: 1 gctctagaatgaacggtgg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 40 seqs, 411 residues

Total number of hits satisfying chosen parameters: 80

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 55 summaries

Database : rni9.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	1	US-08-770-565-9
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4	16.4	86.3	18	1	US-09-721-456-543
5	15	78.9	15	1	US-08-770-565-10
6	11	57.9	11	1	US-08-770-565-11
7	10.2	53.7	13	1	PCT-US94-04361-1
8	10	52.6	10	1	US-09-508-753B-391
9	9.4	49.5	12	1	US-08-390-858B-22
10	8.4	44.2	11	1	US-08-390-858B-3
11	8	42.1	9	1	US-08-642-045B-2
12	8	42.1	9	1	US-09-071-353-4
13	8	42.1	9	1	US-08-852-288-4
14	8	42.1	9	1	US-09-428-346-4
15	8	42.1	10	1	US-08-301-872A-28
16	8	42.1	10	1	US-08-301-872A-28
17	8	42.1	10	1	US-08-244-491A-16
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19	8	42.1	10	1	US-08-161-281A-9
20	8	42.1	10	1	US-08-161-281A-9
21	8	42.1	10	1	US-08-139-882-16
22	8	42.1	10	1	US-08-139-882-16
23	8	42.1	10	1	US-08-797-727A-24
24	8	42.1	10	1	US-08-797-727A-24
25	8	42.1	10	1	US-08-797-727A-25
26	8	42.1	10	1	US-08-797-727A-25
27	8	42.1	10	1	US-08-443-372A-28
28	8	42.1	10	1	US-08-443-372A-28
29	8	42.1	10	1	US-08-189-256A-39
30	8	42.1	10	1	US-08-189-256A-39
31	8	42.1	10	1	US-09-171-878-26
32	8	42.1	10	1	US-09-193-853-39
33	8	42.1	10	1	US-09-193-853-39

34	8	42.1	10	1	US-09-445-283C-64	Sequence 64, Appl
35	7	36.8	8	1	US-08-244-491A-14	Sequence 14, Appl
36	7	36.8	8	1	US-08-244-491A-14	Sequence 14, Appl
37	7	36.8	8	1	US-08-797-727A-22	Sequence 22, Appl
38	7	36.8	8	1	US-08-797-727A-22	Sequence 22, Appl
39	7	36.8	8	1	US-08-650-262-21	Sequence 21, Appl
40	7	36.8	8	1	US-08-650-262-21	Sequence 21, Appl
41	7	36.8	8	1	US-09-171-878-8	Sequence 8, Appl
42	7	36.8	8	1	US-09-171-878-8	Sequence 8, Appl
43	7	36.8	8	1	US-07-845-937A-5	Sequence 5, Appl
44	7	36.8	8	1	US-07-845-937A-5	Sequence 5, Appl
45	7	36.8	8	1	US-09-514-245-43	Sequence 43, Appl
46	6.4	33.7	8	1	US-08-849-075-8	Sequence 8, Appl
47	6.4	33.7	8	1	US-09-286-098-32	Sequence 32, Appl
48	6.4	33.7	8	1	US-09-560-774-99	Sequence 99, Appl
49	6.4	33.7	8	1	US-09-325-193A-26	Sequence 26, Appl
50	6.4	33.7	8	1	US-09-191-170-32	Sequence 32, Appl
51	6.4	33.7	8	1	US-09-684-938-97	Sequence 97, Appl
52	6.4	33.7	8	1	US-09-308-825A-97	Sequence 97, Appl
53	6.4	33.7	8	1	US-09-337-619-95	Sequence 95, Appl
54	6.4	33.7	8	1	US-09-940-244-114	Sequence 114, Appl
55	6	31.6	8	1	US-09-514-245-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-9
; Sequence 9, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-0023000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-9

Query Match 100.0%; Score 19; DB 1; Length 19;

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 09:35:32 ; Search time 0.001 Seconds

(without alignments)
48.564 Million cell updates/sec

Title: US-09-436-060A-9

Perfect score: 19

Sequence: 1 gcttagaatgaacggtgg 19

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 0.5

Searched: 95 seqs, 1278 residues

Total number of hits satisfying chosen parameters: 190

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 101 summaries

Database : rng9.seq *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	1	RNA component of h
2	19	100.0	21	1	ADF33824
3	19	100.0	21	1	Human TERC chimica
4	19	100.0	21	1	Human TERC chimica
5	19	100.0	21	1	Human TERC chimica
6	19	100.0	21	1	Human TERC chimica
7	19	100.0	21	1	hTR-targeted siNA
8	19	100.0	23	1	Human TERC mRNA tr
9	19	100.0	23	1	Human TERC mRNA tr
10	19	100.0	23	1	Human TERC chimica
11	19	100.0	23	1	Human TERC chimica
12	19	100.0	23	1	hTR-targeted siNA
13	19	100.0	23	1	hTR siNA-target RN
14	19	100.0	25	1	hTR siNA-target RN
15	17	89.5	21	1	Human telomerase R
16	17	89.5	21	1	Human telomerase R
17	17	89.5	21	1	Human TERC chimica
18	17	89.5	21	1	Human TERC chimica
19	17	89.5	21	1	Human TERC chimica
20	15	78.9	21	1	hTR-targeted siNA
21	14	73.7	15	1	RNA component of h
22	13	68.4	13	1	Human telomerase p
23	11	57.9	11	1	Human telomerase p
24	11	57.9	11	1	RNA component of h
25	10.4	54.7	12	1	Human telomerase p
26	10.4	54.7	12	1	Human telomerase p
27	10.4	54.7	12	1	Oligonucleotide pr
28	10.4	54.7	13	1	Oligonucleotide pr
29	10.4	54.7	13	1	Synthetic lucifera
30	10.4	54.7	13	1	Oligonucleotide SE
31	10.4	54.7	13	1	Oligonucleotide SE
32	10.4	54.7	13	1	Oligonucleotide SE
33	10.4	54.7	13	1	Oligonucleotide SE

ALIGNMENTS

C 34	10.4	54.7	13	1	ABH46945
C 35	10.4	54.7	13	1	ABF98323
C 36	10.4	54.7	13	1	ABC95736
C 37	10.4	54.7	13	1	ABF87423
C 38	10.2	53.7	13	1	ABF72951
C 39	10.2	53.7	13	1	ABF72951
C 40	10	52.6	12	1	ABF72951
C 41	10	52.6	12	1	ABF72951
C 42	10	52.6	13	1	ABF72951
C 43	9.8	51.6	13	1	ABF72951
C 44	9.8	51.6	13	1	ABF72951
C 45	9.8	51.6	13	1	ABF72951
C 46	9.4	49.5	11	1	ABF72951
C 47	9.4	49.5	11	1	ABF72951
C 48	9.4	49.5	11	1	ABF72951
C 49	9.4	49.5	11	1	ABF72951
C 50	9.4	49.5	12	1	ABF72951
C 51	9.4	49.5	12	1	ABF72951
C 52	9.4	49.5	12	1	ABF72951
C 53	9	47.4	10	1	ABF72951
C 54	9	47.4	10	1	ABF72951
C 55	9	47.4	11	1	ABF72951
C 56	9	47.4	11	1	ABF72951
C 57	9	47.4	12	1	ABF72951
C 58	9	47.4	12	1	ABF72951
C 59	9	47.4	12	1	ABF72951
C 60	9	47.4	12	1	ABF72951
C 61	9	47.4	12	1	ABF72951
C 62	8.4	44.2	10	1	ABF72951
C 63	8.4	44.2	10	1	ABF72951
C 64	8.4	44.2	10	1	ABF72951
C 65	8.4	44.2	10	1	ABF72951
C 66	8.4	44.2	10	1	ABF72951
C 67	8.4	44.2	11	1	ABF72951
C 68	8.4	44.2	11	1	ABF72951
C 69	8.4	44.2	11	1	ABF72951
C 70	8.4	44.2	11	1	ABF72951
C 71	8.4	44.2	11	1	ABF72951
C 72	8.4	44.2	11	1	ABF72951
C 73	8.4	44.2	11	1	ABF72951
C 74	8.4	44.2	11	1	ABF72951
C 75	8	42.1	10	1	ABF72951
C 76	8	42.1	10	1	ABF72951
C 77	8	42.1	10	1	ABF72951
C 78	8	42.1	10	1	ABF72951
C 79	8	42.1	10	1	ABF72951
C 80	8	42.1	10	1	ABF72951
C 81	8	42.1	10	1	ABF72951
C 82	8	42.1	10	1	ABF72951
C 83	8	42.1	10	1	ABF72951
C 84	8	42.1	10	1	ABF72951
C 85	8	42.1	10	1	ABF72951
C 86	8	42.1	10	1	ABF72951
C 87	8	42.1	10	1	ABF72951
C 88	8	42.1	10	1	ABF72951
C 89	8	42.1	10	1	ABF72951
C 90	8	42.1	10	1	ABF72951
C 91	8	42.1	10	1	ABF72951
C 92	8	42.1	10	1	ABF72951
C 93	8	42.1	10	1	ABF72951
C 94	8	42.1	10	1	ABF72951
C 95	8	42.1	10	1	ABF72951
C 96	8	42.1	10	1	ABF72951
C 97	8	42.1	10	1	ABF72951
C 98	8	42.1	10	1	ABF72951
C 99	8	42.1	10	1	ABF72951
C 100	8	42.1	10	1	ABF72951
C 101	8	42.1	10	1	ABF72951

Oligonucleotide SE
Oligonucleotide SE
Oligonucleotide SE
Oligonucleotide SE
Erythropoietin con
Oligonucleotide pr
Human OPAL gene, e
Oligonucleotide SE
Oligonucleotide SE
Oligonucleotide SE
Hepatitis A genome
Human skin EST 532
Human skin EST 256
Human facial skin-
Human facial skin-
Oligonucleotide pr
Oligonucleotide pr
Oligonucleotide pr
Human cholinergic
Yeast NORF gene SA
Human skin EST 900
Human skin EST 158
Oligonucleotide pr
Oligonucleotide pr
Oligonucleotide pr
Oligonucleotide pr
PCR primer used in
Human dendritic ce
Metastatic breast
ISS immunomodulat
Chimeric immunomod
Bcl-2 inhibitory e
Human skin stress/
Human skin EST 551
Human skin EST 439
Human alpha la adr
Human hair-bearing
Human hair-bearing
Xba I linker. Syn
Xba I linker. Syn
Primer used in RAP
Metastatic breast
Metastatic breast
Rabbit GNTI linker
Rabbit GNTI linker
Endoplasmic reticu
Endoplasmic reticu
scFv(ox) antibody
scFv(ox) antibody
Anaerobically-indu
Yeast NORF gene SA
Yeast NORF gene SA
Yeast NORF gene SA
Yeast NORF gene SA
Yeast NORF gene SA
Plasmid pRT100/scF
Plasmid pRT100/scF
Human UBE3A gene A
Human CYP2D6 gene
Human glioma endot
Rat VR1 exon id tr

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 09:33:54 ; Search time 0.001 Seconds
(without alignments)
23.636 Million cell updates/sec

Title: US-09-436-060A-9
Perfect score: 19
Sequence: 1 gctctagaatgaacgggtgg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 54 seqs, 622 residues

Total number of hits satisfying chosen parameters: 108

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 70 summaries

Database : rge9.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	1	AR063833
2	19	100.0	19	1	BD023705
3	19	100.0	25	1	BD131326
4	16.4	86.3	18	1	E36993
5	16.4	86.3	18	1	AR390670
6	16.4	86.3	18	1	AR33284
7	16.4	86.3	18	1	AR810578
8	16.4	86.3	18	1	BD11244
9	15	78.9	15	1	AR063834
10	15	78.9	15	1	BD023706
11	11	57.9	11	1	AR063835
12	11	57.9	11	1	BD023707
13	10.4	54.7	12	1	AX456436
14	10	52.6	10	1	AR303666
15	9.4	49.5	11	1	CO836793
16	9.4	49.5	11	1	CO837258
17	9.4	49.5	11	1	AX625521
18	9.4	49.5	11	1	AX628281
19	9.4	49.5	12	1	I50791
20	9	47.4	11	1	AX624540
21	9	47.4	11	1	AX631961
22	8.4	44.2	10	1	BD239277
23	8.4	44.2	10	1	AX592381
24	8.4	44.2	11	1	CO833068
25	8.4	44.2	11	1	CO833189
26	8.4	44.2	11	1	CO835552
27	8.4	44.2	11	1	I50773
28	8.4	44.2	11	1	AX471853
29	8.4	44.2	11	1	AX627357
30	8.4	44.2	11	1	AX628471
31	8	42.1	9	1	A83648
32	8	42.1	9	1	BD106461
33	8	42.1	10	1	A25264

C 34	8	42.1	10	1	A25264
C 35	8	42.1	10	1	AR027091
C 36	8	42.1	10	1	AR027091
C 37	8	42.1	10	1	AR027092
C 38	8	42.1	10	1	AR027092
C 39	8	42.1	10	1	AR027092
C 40	8	42.1	10	1	AR027092
C 41	8	42.1	10	1	AR027092
C 42	8	42.1	10	1	AR027092
C 43	8	42.1	10	1	AR027092
C 44	8	42.1	10	1	AR027092
C 45	8	42.1	10	1	AR027092
C 46	8	42.1	10	1	AR027092
C 47	8	42.1	10	1	AR027092
C 48	8	42.1	10	1	AR027092
C 49	8	42.1	10	1	AR027092
C 50	8	42.1	10	1	AR027092
C 51	8	42.1	10	1	AR027092
C 52	8	42.1	10	1	AR027092
C 53	8	42.1	10	1	AR027092
C 54	8	42.1	10	1	AR027092
C 55	8	42.1	10	1	AR027092
C 56	8	42.1	10	1	AR027092
C 57	8	42.1	10	1	AR027092
C 58	8	42.1	10	1	AR027092
C 59	8	42.1	10	1	AR027092
C 60	8	42.1	10	1	AR027092
C 61	8	42.1	10	1	AR027092
C 62	8	42.1	10	1	AR027092
C 63	8	42.1	10	1	AR027092
C 64	8	42.1	10	1	AR027092
C 65	8	42.1	10	1	AR027092
C 66	8	42.1	10	1	AR027092
C 67	8	42.1	10	1	AR027092
C 68	8	42.1	10	1	AR027092
C 69	8	42.1	10	1	AR027092
C 70	8	42.1	10	1	AR027092

ALIGNMENTS

RESULT 1	AR063833	Sequence 9 from patent US 5846723.	19 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR063833	Sequence 9 from patent US 5846723.	19 bp	DNA	linear	PAT 29-SEP-1999
DEFINITION	AR063833	Sequence 9 from patent US 5846723.	19 bp	DNA	linear	PAT 29-SEP-1999
ACCESSION	AR063833	Sequence 9 from patent US 5846723.	19 bp	DNA	linear	PAT 29-SEP-1999
VERSION	AR063833.1	GI:5993141	19 bp	DNA	linear	PAT 29-SEP-1999
KEYWORDS	AR063833	Sequence 9 from patent US 5846723.	19 bp	DNA	linear	PAT 29-SEP-1999
SOURCE	AR063833	Sequence 9 from patent US 5846723.	19 bp	DNA	linear	PAT 29-SEP-1999
ORGANISM	AR063833	Sequence 9 from patent US 5846723.	19 bp	DNA	linear	PAT 29-SEP-1999
REFERENCE	AR063833	Sequence 9 from patent US 5846723.	19 bp	DNA	linear	PAT 29-SEP-1999
AUTHORS	AR063833	Sequence 9 from patent US 5846723.	19 bp	DNA	linear	PAT 29-SEP-1999
TITLE	AR063833	Sequence 9 from patent US 5846723.	19 bp	DNA	linear	PAT 29-SEP-1999
JOURNAL	AR063833	Sequence 9 from patent US 5846723.	19 bp	DNA	linear	PAT 29-SEP-1999
FEATURES	AR063833	Sequence 9 from patent US 5846723.	19 bp	DNA	linear	PAT 29-SEP-1999
Query Match	AR063833	Sequence 9 from patent US 5846723.	19 bp	DNA	linear	PAT 29-SEP-1999
Best Local Similarity	AR063833	Sequence 9 from patent US 5846723.	19 bp	DNA	linear	PAT 29-SEP-1999
Mismatches	AR063833	Sequence 9 from patent US 5846723.	19 bp	DNA	linear	PAT 29-SEP-1999
Conservative	AR063833	Sequence 9 from patent US 5846723.	19 bp	DNA	linear	PAT 29-SEP-1999
Indels	AR063833	Sequence 9 from patent US 5846723.	19 bp	DNA	linear	PAT 29-SEP-1999
Gaps	AR063833	Sequence 9 from patent US 5846723.	19 bp	DNA	linear	PAT 29-SEP-1999

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:29:42 ; Search time 0.001 Seconds
(without alignments)
8.880 Million cell updates/sec

Title: US-09-436-060A-10
Perfect score: 15
Sequence: 1 gctctagaatgaacg 15

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 34 seqs, 296 residues

Total number of hits satisfying chosen parameters: 68

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 39 summaries

Database : rnpb10.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	8.4	56.0	10	1	US-10-033-145-695
C 2	8.4	56.0	11	1	US-10-450-797-1430
C 3	8	53.3	8	1	US-10-027-632-52787
C 4	8	53.3	8	1	US-10-027-632-52787
C 5	8	53.3	9	1	US-10-027-632-70835
C 6	8	53.3	9	1	US-10-027-632-70835
C 7	8	53.3	9	1	US-10-345-859-4
C 8	8	53.3	10	1	US-10-663-241-64
C 9	7.6	50.7	10	1	US-10-027-632-81746
C 10	7.6	50.7	10	1	US-10-027-632-81746
C 11	7.4	49.3	9	1	US-10-310-294-22
C 12	7.4	49.3	9	1	US-10-182-327-131
C 13	7.4	49.3	9	1	US-10-669-841-11237
C 14	7.4	49.3	9	1	US-10-673-938-154
C 15	7	46.7	7	1	US-10-310-294-16
C 16	7	46.7	7	1	US-10-310-294-16
C 17	7	46.7	8	1	US-10-669-841-11231
C 18	7	46.7	8	1	US-10-160-232-57
C 19	7	46.7	8	1	US-10-160-232-57
C 20	7	46.7	8	1	US-10-310-294-17
C 21	7	46.7	8	1	US-10-310-294-20
C 22	7	46.7	8	1	US-10-425-668-9
C 23	7	46.7	8	1	US-10-425-668-9
C 24	7	46.7	8	1	US-10-682-420-43
C 25	7	46.7	8	1	US-10-409-613-43
C 26	7	46.7	8	1	US-10-442-180-43
C 27	7	46.7	8	1	US-10-669-841-11232
C 28	7	46.7	8	1	US-10-669-841-11235
C 29	7	46.7	9	1	US-10-757-345-60
C 30	7	46.7	9	1	US-10-310-294-21
C 31	7	46.7	9	1	US-10-310-294-24
C 32	7	46.7	9	1	US-10-310-294-83
C 33	7	46.7	9	1	US-10-310-294-107
C 34	7	46.7	9	1	US-10-669-841-11236

C 34 7 46.7 9 1 US-10-669-841-11239 Sequence 11239, A
C 35 7 46.7 9 1 US-10-669-841-11238 Sequence 11238, A
C 36 7 46.7 9 1 US-10-669-841-11321 Sequence 11321, A
C 37 6 40.0 8 1 US-10-682-420-43 Sequence 43, Appl
C 38 6 40.0 8 1 US-10-409-613-43 Sequence 43, Appl
C 39 6 40.0 8 1 US-10-442-180-43 Sequence 43, Appl

ALIGNMENTS

RESULT 1

US-10-033-145-695/c
; Sequence 695, Application US/10033145
; Publication No. US2002015151SA1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: G80201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 695
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-695

Query Match 56.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTCTAGAATG 11
DB 10 CTCTGAATG 1

RESULT 2

US-10-450-797-1430/c
; Sequence 1430, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1430
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1430

Query Match 56.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGAATGAACG 15
DB 10 AGAATGAACG 1

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:28:22 : Search time 0.001 Seconds
(without alignments)
8.970 Million cell updates/sec

Title: US-09-436-060A-10
Perfect score: 15
Sequence: 1 gctctagaatgaacg 15

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 0.5

Searched: 30 seqs, 299 residues

Total number of hits satisfying chosen parameters: 60

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : rni10.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15	100.0	15	1	US-08-770-565-10
2	15	100.0	19	1	US-08-770-565-9
3	11	73.3	11	1	US-08-770-565-11
4	10.2	68.0	13	1	PCR-US94-04361-1
5	9.4	62.7	12	1	US-08-390-858B-22
6	8.4	56.0	11	1	US-08-390-858B-3
7	8	53.3	9	1	US-09-071-353-4
8	8	53.3	9	1	US-09-426-326-4
9	8	53.3	10	1	US-08-301-872A-28
10	8	53.3	10	1	US-08-301-872A-28
11	8	53.3	10	1	US-08-244-491A-16
12	8	53.3	10	1	US-08-244-491A-16
13	8	53.3	10	1	US-08-161-281A-9
14	8	53.3	10	1	US-08-161-281A-9
15	8	53.3	10	1	US-08-139-862-16
16	8	53.3	10	1	US-08-139-862-16
17	8	53.3	10	1	US-08-797-727A-24
18	8	53.3	10	1	US-08-797-727A-24
19	8	53.3	10	1	US-08-797-727A-25
20	8	53.3	10	1	US-08-797-727A-25
21	8	53.3	10	1	US-08-443-372A-28
22	8	53.3	10	1	US-08-443-372A-28
23	8	53.3	10	1	US-08-189-256A-39
24	8	53.3	10	1	US-08-189-256A-39
25	8	53.3	10	1	US-09-171-878-26
26	8	53.3	10	1	US-09-193-853-39
27	8	53.3	10	1	US-09-193-853-39
28	7	46.7	8	1	US-09-445-283C-64
29	7	46.7	8	1	US-08-244-491A-14
30	7	46.7	8	1	US-08-244-491A-14
31	7	46.7	8	1	US-08-797-727A-22
32	7	46.7	8	1	US-08-797-727A-22
33	7	46.7	8	1	US-08-650-262-21

c	34	7	46.7	8	1	US-08-650-262-21	Sequence 21, Appl
c	35	7	46.7	8	1	US-09-171-878-8	Sequence 8, Appl
c	36	7	46.7	8	1	US-09-171-878-8	Sequence 8, Appl
c	37	7	46.7	8	1	US-07-845-937A-5	Sequence 5, Appl
c	38	7	46.7	8	1	US-07-845-937A-5	Sequence 5, Appl
c	39	7	46.7	8	1	US-09-514-245-43	Sequence 43, Appl
c	40	7	46.7	9	1	US-08-642-045B-2	Sequence 2, Appl
c	41	7	46.7	9	1	US-08-852-268-4	Sequence 4, Appl
c	42	6.4	42.7	8	1	US-09-684-938-97	Sequence 97, Appl
c	43	6.4	42.7	8	1	US-09-308-825A-97	Sequence 97, Appl
c	44	6.4	42.7	8	1	US-09-340-244-114	Sequence 114, Appl
c	45	6	40.0	8	1	US-09-514-245-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-10
Sequence 10, Application US/08770565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Fruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-0023000US
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-10

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.32; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;
Qy 1 GCTCTAGATGAACG 15
Db 1 GCTCTAGATGAACG 15

RESULT 2
US-08-770-565-9

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:27:00 ; Search time 0.001 Seconds
(without alignments)
17.490 Million cell updates/sec

Title: US-09-436-060A-10

Perfect score: 15

Sequence: 1 gctctagaatgaacg 15

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 53 seqs, 583 residues

Total number of hits satisfying chosen parameters: 106

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 59 summaries

Database : rng10.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	1 AAV41177	RNA component of h
2	15	100.0	19	1 AAV41176	RNA component of h
3	13	86.7	13	1 AAS15930	Human telomerase p
4	11	73.3	11	1 AAV41178	RNA component of h
5	11	73.3	11	1 AAS15929	Human telomerase p
6	10.4	69.3	12	1 ABL39311	Synthetic luciferase
7	10.2	68.0	13	1 AAV72951	Erythropoietin con
8	10	66.7	12	1 ABL27364	Oligonucleotide pr
9	10	66.7	12	1 ABL72570	Human OPAL Gene, e
10	9.8	65.3	13	1 ADO58258	Hepatitis A Genome
11	9.4	62.7	11	1 ABV67536	Human skin EST 532
12	9.4	62.7	11	1 ADQ34226	Human facial skin-
13	9.4	62.7	12	1 ASH78027	Oligonucleotide pr
14	9	60.0	10	1 AAD05873	Human cholinergic
15	9	60.0	10	1 AAF34756	Yeast NORF gene SA
16	9	60.0	11	1 ABV71216	Human skin EST 900
17	9	60.0	11	1 ABV63795	Human skin EST 158
18	9	60.0	12	1 ASI77502	Oligonucleotide pr
19	9	60.0	12	1 ASI50973	Oligonucleotide pr
20	9	60.0	12	1 ASI34553	Oligonucleotide pr
21	9	60.0	12	1 ASH82778	Oligonucleotide pr
22	9	60.0	12	1 AB167594	Oligonucleotide pr
23	8.4	56.0	10	1 AAZ78267	Human dendritic ce
24	8.4	56.0	10	1 AAZ83713	Metastatic breast
25	8.4	56.0	11	1 AAT79837	Bcl-2 inhibitory e
26	8.4	56.0	11	1 AAG87675	Human skin stress/
27	8.4	56.0	11	1 ABV64776	Human skin EST 256
28	8.4	56.0	11	1 ABV67726	Human skin EST 551
29	8.4	56.0	11	1 ABV66612	Human skin EST 439
30	8.4	56.0	11	1 ADO80074	Human alpha la adr
31	8.4	56.0	11	1 ADQ32520	Human facial skin-
32	8.4	56.0	11	1 ADQ33761	Human facial skin-
33	8	53.3	10	1 AAQ98160	Xba I linker. Syn

C 34	8	53.3	10	1	AAQ98160	Xba I linker. Syn
C 35	8	53.3	10	1	AAV35994	Primer used in RAP
C 36	8	53.3	10	1	AAZ85884	Metastatic breast
C 37	8	53.3	10	1	AAZ86135	Metastatic breast
C 38	8	53.3	10	1	AAH48687	Rabbit GNTI linker
C 39	8	53.3	10	1	AAH48687	Rabbit GNTI linker
C 40	8	53.3	10	1	AAH49493	Endoplasmic reticu
C 41	8	53.3	10	1	AAH49493	Endoplasmic reticu
C 42	8	53.3	10	1	AAH49475	scFv(ox) antibody
C 43	8	53.3	10	1	AAH49475	scFv(ox) antibody
C 44	8	53.3	10	1	AAH20937	Anaerobically-indu
C 45	8	53.3	10	1	AAH20937	Anaerobically-indu
C 46	8	53.3	10	1	AAH41400	Yeast NORF gene SA
C 47	8	53.3	10	1	AAH43641	Yeast NORF gene SA
C 48	8	53.3	10	1	AAH43641	Yeast NORF gene SA
C 49	8	53.3	10	1	AAH436297	Yeast NORF gene SA
C 50	8	53.3	10	1	AAH43592	Yeast NORF gene SA
C 51	8	53.3	10	1	AAH40628	Yeast NORF gene SA
C 52	8	53.3	10	1	AAH41401	Yeast NORF gene SA
C 53	8	53.3	10	1	AAI69335	Plasmid pRT100/scF
C 54	8	53.3	10	1	AAI69335	Plasmid pRT100/scF
C 55	8	53.3	10	1	ABL45711	Human UBE3A gene A
C 56	8	53.3	10	1	ABQ72361	Human CYP2D6 gene
C 57	8	53.3	10	1	ADK12856	Human glioma endot
C 58	7.4	49.3	9	1	AAH70112	Sequence capable o
C 59	7.4	49.3	9	1	ACD56699	HBV RT primer deco

ALIGNMENTS

RESULT 1

AAV41177

ID AAV41177 standard; DNA; 15 BP.

XX AC AAV41177;

XX XX

DT 08-OCT-1998 (first entry)

XX XX

DE RNA component of human telomerase (hTR) antisense oligo 21ab3.

XX RNA component; human telomerase; antisense oligonucleotide; infection;
neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
contraception; sterilization; immunosuppression; therapeutic; hTR;
immune system down-regulation; anti-inflammatory therapy; ss.

OS Synthetic.

OS Homo sapiens.

XX WO9828442-A1.

XX PD 02-JUL-1998.

XX PF 19-DEC-1997; 97WO-US023619.

XX PR 20-DEC-1996; 96US-00770564.

XX PR 20-DEC-1996; 96US-00770565.

XX PA (GERO-) GERON CORP.

XX Kim NW, Wu F, Kealey JT, Pruzan R, Weinrich SL;

XX WPI; 1998-377670/32.

XX PT New polynucleotide(s) antisense to human telomerase - used for detecting

XX or inhibiting human telomerase, e.g. for treating cancers, contraception,

XX immuno-suppression or treating infection.

XX PS Claim 11; Page 65; 80pp; English.

XX CC Sequences shown in AAV41189 to AAV41181 represent antisense

XX oligonucleotides to the RNA component of human telomerase (hTR). These

XX antisense oligonucleotides specifically hybridize to a nucleotide

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:19:42, Search time 0.001 Seconds
(without alignments)
13.650 Million cell updates/sec

Title: US-09-436-060A-10

Perfect score: 15

Sequence: 1 gctctagaatgaacg 15

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 0.5

Searched: 43 seqs, 455 residues

Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 7

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 59 summaries

Database: rge10.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	1	AR063834
2	15	100.0	15	1	BD023706
3	15	100.0	19	1	AR063833
4	15	100.0	19	1	BD023705
5	11	73.3	11	1	AR063835
6	11	73.3	11	1	BD023707
7	10.4	69.3	12	1	AX456436
8	9.4	62.7	11	1	CQ837258
9	9.4	62.7	11	1	AX628281
10	9.4	62.7	12	1	I50791
11	9	60.0	11	1	AX624540
12	9	60.0	11	1	AX631961
13	8.4	56.0	10	1	BD239277
14	8.4	56.0	11	1	CQ835552
15	8.4	56.0	11	1	CQ836793
16	8.4	56.0	11	1	I50773
17	8.4	56.0	11	1	AX471853
18	8.4	56.0	11	1	AX625521
19	8.4	56.0	11	1	AX627357
20	8.4	56.0	11	1	AX628471
21	8	53.3	9	1	A83648
22	8	53.3	9	1	BD106461
23	8	53.3	10	1	A25264
24	8	53.3	10	1	A25264
25	8	53.3	10	1	AR027091
26	8	53.3	10	1	AR027091
27	8	53.3	10	1	AR027092
28	8	53.3	10	1	AR027092
29	8	53.3	10	1	AR032385
30	8	53.3	10	1	AR032385
31	8	53.3	10	1	AR160668
32	8	53.3	10	1	I40153
33	8	53.3	10	1	I40153

34	8	53.3	10	1	I45921
35	8	53.3	10	1	I45921
36	8	53.3	10	1	I89756
37	8	53.3	10	1	I89756
38	8	53.3	10	1	AR403689
39	8	53.3	10	1	AX205086
40	8	53.3	10	1	AX205086
41	8	53.3	10	1	AX259320
42	8	53.3	10	1	AX259320
43	7.4	49.3	9	1	BD023708
44	7	46.7	8	1	E17002
45	7	46.7	8	1	E17002
46	7	46.7	8	1	E17034
47	7	46.7	8	1	E17034
48	7	46.7	8	1	E17034
49	7	46.7	8	1	E17045
50	7	46.7	8	1	E17045
51	7	46.7	8	1	E41637
52	7	46.7	8	1	E41637
53	7	46.7	8	1	AX003296
54	7	46.7	8	1	BD092167
55	7	46.7	8	1	BD092167
56	7	46.7	9	1	A70966
57	7	46.7	9	1	S98713
58	6.4	42.7	9	1	A70966
59	6	40.0	8	1	AX003296

ALIGNMENTS

RESULT 1	AR063834	Sequence 10 from patent US 5846723.	15 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR063834					
DEFINITION	AR063834					
ACCESSION	AR063834					
VERSION	AR063834.1	GI:5993142				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 15)					
AUTHORS	Kim N.Woo., Wu F., Kealey J.T., Pruzan R. and Weinrich S.L.					
TITLE	Methods for detecting the RNA component of telomerase					
JOURNAL	Patent: US 5846723-A 10 08-DEC-1998;					
FEATURES	Location/Qualifiers					
source	1..15					
	/organism="unknown"					
	/mol_type="unassigned DNA"					
Query Match	100.0%;	Score 15;	DB 1;	Length 15;		
Best Local Similarity	100.0%;	Pred. No. 0.87;				
Matches	15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1 GCTCTAGATGACG 15					
Db	1 GCTCTAGATGACG 15					
RESULT 2	BD023706	Sequence 15 from patent US 5846723.	15 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD023706					
DEFINITION	BD023706					
ACCESSION	BD023706					
VERSION	BD023706.1	GI:22564929				
KEYWORDS	JP 2001507229-A/10.					
SOURCE	unidentified					
ORGANISM	unidentified					
REFERENCE	1 (bases 1 to 15)					
AUTHORS	Kim N.W., Wu F., Kealey J.T., Pruzan R. and Weinrich S.L.					
TITLE	Method for detecting and inhibiting RNA component of telomerase					
JOURNAL	Patent: JP 2001507229-A 10 05-JUN-2001;					

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:12:40 ; Search time 0.001 Seconds
(without alignments)
5.720 Million cell updates/sec

Title: US-09-436-060A-11
Perfect score: 11
Sequence: 1 GCTCTAGATG 11

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5

Searched: 29 seqs, 260 residues

Total number of hits satisfying chosen parameters: 58

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 47 summaries

Database : rni11.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	1	US-08-770-565-11
2	9.4	85.5	12	1	US-08-390-858B-22
3	8	72.7	9	1	US-09-071-353-4
4	8	72.7	9	1	US-09-426-326-4
5	8	72.7	10	1	US-08-301-872A-28
6	8	72.7	10	1	US-08-301-872A-28
7	8	72.7	10	1	US-08-244-491A-16
8	8	72.7	10	1	US-08-244-491A-16
9	8	72.7	10	1	US-08-161-281A-9
10	8	72.7	10	1	US-08-139-862-16
11	8	72.7	10	1	US-08-139-862-16
12	8	72.7	10	1	US-08-797-727A-24
13	8	72.7	10	1	US-08-797-727A-24
14	8	72.7	10	1	US-08-797-727A-25
15	8	72.7	10	1	US-08-797-727A-25
16	8	72.7	10	1	US-08-443-372A-28
17	8	72.7	10	1	US-08-443-372A-28
18	8	72.7	10	1	US-08-189-356A-39
19	8	72.7	10	1	US-08-189-356A-39
20	8	72.7	10	1	US-08-171-878-26
21	8	72.7	10	1	US-08-171-878-26
22	8	72.7	10	1	US-09-193-853-39
23	8	72.7	10	1	US-09-193-853-39
24	7	63.6	8	1	US-08-244-491A-14
25	7	63.6	8	1	US-08-244-491A-14
26	7	63.6	8	1	US-08-797-727A-22
27	7	63.6	8	1	US-08-797-727A-22
28	7	63.6	8	1	US-08-650-262-21
29	7	63.6	8	1	US-08-650-262-21
30	7	63.6	8	1	US-09-171-878-8
31	7	63.6	8	1	US-09-171-878-8
32	7	63.6	8	1	US-07-845-937A-5
33	7	63.6	8	1	US-07-845-937A-5

34 7 63.6 8 1 US-09-514-245-43 Sequence 43, Appl
35 6.4 58.2 8 1 US-08-684-938-97 Sequence 97, Appl
36 6.4 58.2 8 1 US-09-308-825A-97 Sequence 97, Appl
37 6.4 58.2 8 1 US-09-940-244-114 Sequence 114, Appl
38 6 54.5 7 1 US-09-117-122-2 Sequence 2, Appl
39 6 54.5 8 1 US-09-117-122-2 Sequence 2, Appl
40 6 54.5 8 1 US-09-514-245-43 Sequence 43, Appl
41 6 54.5 8 1 US-09-041-675-1 Sequence 1, Appl
42 6 54.5 8 1 US-09-041-675-1 Sequence 1, Appl
43 6 54.5 8 1 US-09-041-675-16 Sequence 16, Appl
44 6 54.5 8 1 US-09-041-675-16 Sequence 16, Appl
45 6 54.5 8 1 US-08-290-736C-13 Sequence 13, Appl
46 6 54.5 8 1 US-09-054-832-11 Sequence 11, Appl
47 6 54.5 8 1 US-09-640-953-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-11
; Sequence 11, Application US/08770565
; Patent No 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weirich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-0023000US
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-11

Query Match 100.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. NO. 0.38;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTCTAGATG 11

Db 1 GCTCTAGATG 11

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:11:07 ; Search time 0.001 Seconds
(without alignments)
6.446 Million cell updates/sec

Title: US-09-436-060A-11
Perfect score: 11
Sequence: 1 gctctagaatg 11

Scoring table: IDENTITY NUC
Gapop 10_0, Gapext 0.5

Searched: 30 seqs, 293 residues

Total number of hits satisfying chosen parameters: 60

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 42 summaries

Database : rng11.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	1 AAV41178	RNA component of h
2	11	100.0	11	1 AAG15929	Human telomerase p
3	11	100.0	13	1 AAG15930	Human telomerase p
C 4	10	90.9	12	1 ABL99311	Synthetic lucifera
5	9	81.8	10	1 AAF34756	Yeast NORF gene SA
C 6	8.4	76.4	10	1 AAZ78267	Human dendritic ce
C 7	8.4	76.4	11	1 ABV66612	Human skin ESR 439
C 8	8.4	76.4	11	1 ADQ32520	Human facial skin-
9	8	72.7	10	1 AAQ98160	Xba I linker. Syn
C 10	8	72.7	10	1 AAQ98160	Xba I linker. Syn
C 11	8	72.7	10	1 AAV35994	Primer used in RAP
12	8	72.7	10	1 AAZ36584	Metastatic breast
13	8	72.7	10	1 AAZ36135	Metastatic breast
14	8	72.7	10	1 AAH48687	Rabbit Gnrl linker
C 15	8	72.7	10	1 AAH48687	Rabbit Gnrl linker
16	8	72.7	10	1 AAH49493	Endoplasmic reticu
C 17	8	72.7	10	1 AAH49493	Endoplasmic reticu
18	8	72.7	10	1 AAH49475	scFv(ox) antibody
C 19	8	72.7	10	1 AAH49475	scFv(ox) antibody
20	8	72.7	10	1 AAH20937	Anaerobically-indu
C 21	8	72.7	10	1 AAH20937	Anaerobically-indu
22	8	72.7	10	1 AAF41400	Yeast NORF gene SA
C 23	8	72.7	10	1 AAF41399	Yeast NORF gene SA
24	8	72.7	10	1 AAF36297	Yeast NORF gene SA
C 25	8	72.7	10	1 AAF41401	Yeast NORF gene SA
26	8	72.7	10	1 AAI69335	Plasmid pRT100/scF
C 27	8	72.7	10	1 AAI69335	Plasmid pRT100/scF
C 28	8	72.7	10	1 ABQ72361	Human CYP2D6 gene
29	7	63.6	7	1 AAV41179	RNA component of h
C 30	7	63.6	8	1 AAZ87757	Anti-human VEGF re
C 31	7	63.6	8	1 AAZ87757	Anti-human VEGF re
32	7	63.6	8	1 AAF70230	Flt-1 related DNA
C 33	7	63.6	8	1 AAF70230	Flt-1 related DNA

34 7 63.6 8 1 ABK29963 Hepatitis B virus
C 35 7 63.6 8 1 ABK29963 Hepatitis B virus
C 36 7 63.6 9 1 AAV28804 Primer extension p
C 37 7 63.6 10 1 AAF34756 Yeast NORF gene SA
C 38 6.4 58.2 8 1 AAT76716 Miniprobe oligonuc
C 39 6.4 58.2 8 1 AAV65875 Miniprobe oligonuc
C 40 6.4 58.2 8 1 ABK29965 Hepatitis B virus
C 41 6.4 58.2 9 1 AAV28804 Primer extension p
C 42 6 54.5 8 1 ABK29965 Hepatitis B virus

ALIGNMENTS

RESULT 1
AAV41178
ID AAV41178 standard; DNA; 11 BP.
XX
AC AAV41178;
XX
DT 08-OCT-1998 (first entry)
XX
DE RNA component of human telomerase (hTR) antisense oligo 21ab2.
XX
KW RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW contraception; sterilisation; immunosuppression; therapeutic; hTR;
KW immune system down-regulation; anti-inflammatory therapy; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FN W09828442-A1.
XX
PD 02-JUL-1998.
XX
PF 19-DEC-1997; 97WO-US023619.
XX
PR 20-DEC-1996; 96US-00770564.
PR 20-DEC-1996; 96US-00770565.
XX
(GERO-) GERON CORP.
XX
KIm NW, Wu F, Kealey JT, Pruzan R, Weinrich SL;
XX
WPI: 1998-377670/32.
XX
New polynucleotide(s) anti:sense to human telomerase - used for detecting
or inhibiting human telomerase, e.g. for treating cancers, contraception,
immuno-suppression or treating infection.
XX
Claim 11; Page 65; 80pp; English.

Sequences shown in AAV41169 to AAV41181 represent antisense
oligonucleotides to the RNA component of human telomerase (hTR). These
antisense oligonucleotides specifically hybridise to a nucleotide
sequence within an accessible region of the hTR, but that does not
hybridise to a sequence within the template region of hTR. These
oligonucleotides may specifically be used for detection of an RNA
component of human telomerase in a sample. This is useful for diagnosing
cancer (especially neuroblastoma, bladder, colon and prostate cancer),
and providing prognosis for a cancer patient. The inhibitory
oligonucleotides can inhibit the telomerase activity level in a cell by
interfering with transcription of the RNA component, decreasing the half-
life of the telomerase RNA component transcript, inhibiting assembly of
the RNA component into the telomerase holoenzyme, or inhibiting the
polymerase activity of telomerase. These antisense oligonucleotides can
be used for inhibiting telomerase activity in both cultured cells and in
cells in vivo. They can be used in therapeutics for treating or
preventing cancer, for contraception or sterilisation, for
immunosuppression, and for selectively down-regulating specific branches
of the immune system, e.g. a specific subset of T-cells, in anti-
inflammatory therapies or for treating infections by, e.g. yeast.

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OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 08:08:37 ; Search time 0.001 Seconds
(without alignments)
7.150 Million cell updates/sec

Title: US-09-436-060A-11

Perfect score: 11
Sequence: 1 gctctagaatg 11

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 35 seqs, 325 residues

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 7
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 53 summaries

Database : rgell.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	11	1	AR063835
2	11	100.0	11	1	BD023707
3	10	90.9	12	1	AX456436
4	9.4	85.5	12	1	AX456436
5	8.4	76.4	10	1	AX0791
6	8.4	76.4	11	1	BD239277
7	8.4	76.4	11	1	AX035552
8	8.4	76.4	11	1	AX627357
9	8	72.7	9	1	AX3648
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32	8	72.7	10	1	AR027092
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C 35 7 63.6 8 1 E17045
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C 37 7 63.6 8 1 E1637
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C 42 7 63.6 9 1 S98713
C 43 6.4 58.2 8 1 AX059000
44 6.4 58.2 8 1 AX059001
45 6.4 58.2 9 1 A70966
46 6.2 56.4 8 1 AX059000
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50 6 54.5 8 1 BD260031
51 6 54.5 8 1 E13216
52 6 54.5 8 1 AX687098
C 53 6 54.5 8 1 AX687099

ALIGNMENTS

RESULT 1
AR063835
LOCUS
DEFINITION Sequence 11 from patent US 5846723.
ACCESSION AR063835
VERSION AR063835.1 GI:5993143
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 11)

AUTHORS Kim, N.Woo., Wu, F., Kealey, J.T., Pruzan, R. and Weinrich, S.L.

TITLE Methods for detecting the RNA component of telomerase

JOURNAL Patent: US 5846723-A 11 08-DEC-1998;

FEATURES
Location/Qualifiers
1..11

source

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 100.0%; Score 11; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGAATG 11

Db 1 GCTCTAGAATG 11

RESULT 2

BD023707

LOCUS

DEFINITION Method for detecting and inhibiting RNA component of telomerase.

ACCESSION BD023707

VERSION BD023707.1 GI:22564930

KEYWORDS JP 2001507229-A/11.

SOURCE unidentified

ORGANISM unclassified

REFERENCE 1 (bases 1 to 11)

AUTHORS Kim, N.W., Wu, F., Kealey, J.T., Pruzan, R. and Weinrich, S.L.

TITLE Method for detecting and inhibiting RNA component of telomerase

JOURNAL Patent: JP 2001507229-A 11 05-JUN-2001;

COMMENT GERON CORP

PD JP 2001507229-A/11

PN 05-JUN-2001

PF 19-DEC-1997 JP 1998529003

PR 20-DEC-1996 US 08/770564, 20-DEC-1996 US 08/770565 PI

NAM WOO KIM, FRED WU, JAMES T KEALEY, RONALD PRUZAN, SCOTT L PI